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OM nucleic - nucleic search, using sw model

Run on: September 21, 2005, 23:55:17 ; Search time 373 Seconds
(without alignments)
7198.740 Million cell updates/sec

Title: US-09-943-857A-3

Perfect score: 1641

Sequence: 1 tcgatgaattcacgtggccc.....accgctcttcttttctgtg 1641

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A-COMB.seq:*

2: /cgn2_6/prodata/1/ina/5B-COMB.seq:*

3: /cgn2_6/prodata/1/ina/6A-COMB.seq:*

4: /cgn2_6/prodata/1/ina/6B-COMB.seq:*

5: /cgn2_6/prodata/1/ina/PCTUS-COMB.seq:*

6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1248.8	76.1	1650	2	US-08-776-210-6
2	337.8	20.6	1828	3	US-08-362-525-11
3	332.2	20.2	1635	2	US-08-776-210-5
4	264.6	16.1	2045	1	US-08-379-926A-7
5	151.6	9.2	8533	1	US-07-846-181-6
6	151.6	9.2	8533	1	US-07-845-989-6
7	119.6	7.3	1738	2	US-08-932-378A-1
8	75.8	4.6	1572	4	US-09-902-540-2451
9	75.8	4.6	14484	4	US-09-902-540-1108
10	74.4	4.5	1725	4	US-09-810-861B-5
11	74.4	4.5	1845	1	US-07-732-962A-1
12	74.4	4.5	1845	5	PCT-US92-06106-1
13	74.4	4.5	2158	4	US-09-949-016-1192
14	74.4	4.5	2158	4	US-09-949-016-1193
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16	74.4	4.5	2256	3	US-08-370-156-1
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18	74.4	4.5	3016	2	US-08-318-826A-7
19	74.4	4.5	3016	2	US-08-370-156-5
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21	74.4	4.5	3096	2	US-08-318-826A-6
22	74.4	4.5	3096	2	US-08-370-156-3
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25	74.4	4.5	14446	4	US-09-810-861B-4
26	73.6	4.5	2184	1	US-08-445-050-8
27	73.6	4.5	2184	1	US-08-204-691-8

28 73.6 4.5 2375 4 US-09-949-016-3976
29 73.6 4.5 2428 1 US-08-445-050-1
30 73.6 4.5 2428 1 US-08-204-691-1
31 73.6 4.5 2428 4 US-09-355-295B-2
32 73.6 4.5 2487 3 US-08-370-223-12
33 73 4.4 9885 4 US-09-949-016-12934
34 73 4.4 9885 4 US-09-949-016-12935
35 73 4.4 35060 3 US-08-814-095-7
36 72 4.4 2344 3 US-09-347-878-31
37 72 4.4 2734 4 US-09-569-611C-5
38 72 4.4 2781 4 US-09-569-611C-6
39 72 4.4 3018 1 US-08-347-718B-3
40 72 4.4 3018 1 US-08-482-262-3
41 72 4.4 3018 6 5200183-1
42 72 4.4 3018 6 5200183-1
43 70.2 4.3 2117 4 US-09-949-016-3799
44 70.2 4.3 2169 4 US-09-949-016-555
45 70.2 4.3 2191 4 US-09-595-682B-27

ALIGNMENTS

RESULT 1
US-08-776-210-6
; Sequence 6, Application US/08776210
; Patent No. 5942659
; GENERAL INFORMATION:
; APPLICANT: ALIBERT, Gilbert
; APPLICANT: MOULOUNGUI, Zephirin
; APPLICANT: BOUDET, Alain
; TITLE OF INVENTION: PROCESS FOR PRODUCING FATTY ACIDS OR
; TITLE OF INVENTION: DERIVATIVES THEREOF FROM OLEAGINOUS PLANTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,210
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 09272
; FILING DATE: 25-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00957
; FILING DATE: 18-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: IN 387 - BE 6996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-776-210-6

Sequence 3976, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 12934, A
Sequence 12935, A
Sequence 7, Appli
Sequence 31, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 3, Appli
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Patent No. 5200183
Patent No. 5200183
Sequence 3799, Ap
Sequence 555, App
Sequence 27, Appli

Query Match				76.1%;	Score 1248.8;	DB 2;	Length 1650;
Best Local Similarity				86.2%;	Pred. No. 1.1e-293;	Indels	0; Gaps 0;
Matches 1382;				Conservative	0;	Mismatches 222;	Indels 0; Gaps 0;
QY	38	CGGTATCCACCGCCAGCTCGCCAAAGCGGACACCATCACCGGTCTCAACGCGCATCATCA	97				
DB	44	CTGCCCCACCGCCAGCTCGCCAAAGCGGACACCATCACCGGTCTCAACGCGCATCATCA	103				
QY	98	ACGAGCGGTCTCTCGGCATTCCTTTTCCGAGCGCGCGGTGGGCAACCTTCGCGTCAAGG	157				
DB	104	ACGAGCGGTCTCTCGGCATTCCTTTTCCGAGCGCGCGGTGGGCAACCTTCGCGTCAAGG	163				
QY	158	ACCTGTGCGTACTCTGCTCGCTCAACGCGGACAGATTCACTTCTTACGCGCGTCTT	217				
DB	164	ACCTGTGCGTACTCTGCTCGCTCAACGCGGACAGATTCACTTCTTACGCGCGTCTT	223				
QY	218	GCATGACGAGAACCCCGAGGGGACGTTTGAAGAGAACCTTGGCAAGACGGCACTCGACT	277				
DB	224	GCATGACGAGAACCCCGAGGGGACCTTACGAGAGAACCTTCCCAAGGACGCGCTCGACT	283				
QY	278	TGCTGATGACGTCCAAAGTGTTCAGGCGGTGCTTCCAGAGTGAGAGTGCCTCACCA	337				
DB	284	TGCTGATGACGTCCAAAGTGTTCAGGCGGTGCTTCCAGAGTGAGAGTGCCTCACCA	343				
QY	338	TCAAAGTGTGCGGCGCGGCGCACCAAGGCGGCGCCCAACCTTCCCGGTTCATGCTCTGA	397				
DB	344	TCAAAGTGTGCGGCGCGGCGCACCAAGGCGGCGCCCAACCTTCCCGGTTCATGCTCTGA	403				
QY	398	TCTTTTGGCGGTGGTGTGAGATCGGCAGCCCAACCATCTTCCCTCCCGCCAGATGGTCA	457				
DB	404	TCTTTTGGCGGTGGTGTGAGTGGGTGGGCACGACCATCTTCCCTCCCGCCAGATGATCA	463				
QY	458	CAAAGATGTCTCATGGGCAAGACATCATCTCAAGTGGCCGTCAACTACCGTGTGCTT	517				
DB	464	CAAAGATGTCTCATGGGCAAGCCCATCATCTCAAGTGGCCGTCAACTACCGCGTGTCT	523				
QY	518	CTGGGGGTCTCTGGCTGTGTGATGATCAATCAAGCGCGGAGCGGAGCGCGCTTGA	577				
DB	524	CTGGGGGTCTCTGGCTGTGTGAGATGATCAATCAAGCGCGGAGCGGAGCGCGCTTGA	583				
QY	578	AGGACAGCGTTTGGGATGATGAGTGGGTGGGACAAACATTCGCGGTTTGGCGCGACC	637				
DB	584	AGGACAGCGTTTGGGATGATGAGTGGGTGGGACAAACATTCGCGGTTTGGCGCGACC	643				
QY	638	CGAGCAAGTGTACTATCTTGGCGAGTCTGCGGCGAGCATGTCCGTGTGTCACCTCA	697				
DB	644	CGACCAAGTGTACTATCTTGGCGAGTCTGCGGCGAGCATGTCCGTGTGTCACCTTC	703				
QY	698	TCGTGAACGACGCGGACACGATACAGGCGAAGCGGTGTTCGCGCGGCGCATCATGC	757				
DB	704	TCGTGAACGACGCGGACACGATACAGGCGAAGCGGTGTTCGCGCGGCGCATCATGC	763				
QY	758	AGTCTGGAGCCATGTTGCGCTCTGACCCCGGTGGAGCGGACGTCACGCGCAACGAGATCTACG	817				
DB	764	AGTCTGGAGCCATGTTGCGCTCTGACCCCGGTGGAGCGGACGTCACGCGCAACGAGATCTTGTG	823				
QY	818	ACCTCTTTGCTCTGAGTGTCTGCTGTGAGCGGCGGACGAGCATGTCCGTGCTTGGCGCA	877				
DB	824	ACCTCTTTGCTCTGAGTGTCTGCTGTGAGCGGCGGACGAGCATGTCCGTGCTTGGCGG	883				
QY	878	GTGCGCTTACGACACCTTGTCTCGATGCGACCAACAACTCTCTGGGTCTTGGCGGTACT	937				
DB	884	GTGCTGTAGCGACAGTGTGGAGGACGCGACCAACAACTCTGGGTCTTGGCGGTACT	943				
QY	938	CTCGTGTGGGTGTGTTTATCTCCCGCGGCGCGAGCGGCAAGAACATCAACGATGACATGT	997				
DB	944	CTCGTGTGGGTGTGTTTATCTCCCGCGGCGCGAGCGGCGTGAACATCAACGAGACATGT	1003				
QY	998	ACAAGTGTGCGGACGCGGAGTATGCAAGGTTCCTCGTGTATCTTGGCGGACGAGAGG	1057				
DB	1004	ACGCTTGTGTCGCGGAGGCAAGTATGCCAAATCTCTGTGATCATCTGCGCGACCGAAGG	1063				
QY	1058	ACGAGGGACCATCTTTTGGGCTCTCTTCTTTGAACGTGACCAACGATGTCTAGGCCCGGTG	1117				

DB	1064	ACGAGGGACCTTCTTTGGCACCCCTGTGTTGAAGCTGACCGATGCCAGGCGCGCGG	1123				
QY	1118	CTTACTTCAAGCAGTCTTTTTCATCCACGCGAGCGAGGATGACACCTTGTATGGCGG	1177				
DB	1124	AGTACTTCAAGCAGTCTTTTGTCCACGCGAGCGAGATCGACACGTTGTATGACGG	1183				
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DB	1184	CGTACCCCGGAGCATCACCCAGGGCTTGGCTTCGACACGGGTATTTCTCAACGCGCTCA	1243				
QY	1238	CCCCGAGTTCAGAGAGAAATCTCTGGGTGCTCGGCGACTTTCATTCATCAACGCGCGG	1297				
DB	1244	CCCCGAGTTCAGAGAGAAATCTCGGCGGTCTCGGCGACTTTCATTCATCAACGCGCTCA	1303				
QY	1298	GCTACTTCTCAACCACTTTCAGGCGGCGACCAAGTACTCGTTCCTCTTAAGCAGCTCT	1357				
DB	1304	GCTACTTCTCAACCACTTTCAGGCGGCGACCAAGTACTCTCTTAAGCAGCTCT	1363				
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DB	1484	CCAAACACCGCGGGTGTGTGTGAAGTGGCGGAGTACACGACGAGCTCTCAGTGTGGA	1543				
QY	1538	ACAACTTGTATGATGATCAACGCGTTCGCTTGGGCTTGTACACCGGCAAGGACAACTTCCGACCG	1597				
DB	1544	ACAACTTGTATGATGATCAACGCGTTCGCTTGGGCTTGTACACCGGCAAGGACAACTTCCGACCG	1603				
QY	1598	CTGGTACGACGCGTGTGATGACCAACCGCTCTTCTTCTTTTGTG	1641				
DB	1604	CGGCTACGACGCGTGTGTTCTTCAACCGCGCTCTTCTTTGTG	1647				

RESULT 2

US-08-362-525-11
; Sequence 11, Application US/08362525
; Patent No. 6027910
; GENERAL INFORMATION:
; APPLICANT: KLIS, FRANCISCUS M.
; APPLICANT: SCHREUDER, MAARTEN P.
; APPLICANT: TOSCHKA, HOLSER Y.
; APPLICANT: VERRIPS, CORNELIS T.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
; TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: CUSHMAN DARBY & CUSHMAN, L.L.P.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,525
; FILING DATE: 04-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92202080.5
; FILING DATE: 08-JUL-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92203899.7
FILING DATE: 14-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/01763
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 213289/T7020 (V)
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA.
ORGANISM: Geotrichum candidum
STRAIN: CMIC 335426
FEATURE:
NAME/KEY: CDS
LOCATION: 40..1731
OTHER INFORMATION: /product= "lipase"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 40..96
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 97..1728
OTHER INFORMATION: /product= "lipase"
OTHER INFORMATION: /gene= "lipb"
US-08-362-525-11

Query Match 20.6%; Score 337.8; DB 3; Length 1828;
Best Local Similarity 54.3%; Pred. No. 2.7e-72;
Matches 815; Conservative 0; Mismatches 647; Indels 39; Gaps 5;

QY 21 AGCGCGCTCTCGGATCGGTACCCACCGCCAAAGCTCGCCCAACGGGACACCATCACCGG 80
DB 81 AGTGGGCACCTTGGGCCAGGCCCCCACGGCCGTTCTTAATGGCAACAGGTCATCTCTGG 140
QY 81 TCTCAAGCGCATCATCAAGAGCGGCTTCTCGGCATTCCTTTCGAGCGCGCGGTGGG 140
DB 141 TGTCTTGGGCAAGGTTGATACCTTCAAGGAATCCCATTTGCTGACCCCTCTGTTGG 200
QY 141 CAACCTCCGCTTCAAGGACCTGTGCGGTACTCTGGCTCGCTCAACGGCCAGAACTTCAAC 200
DB 201 TGACTTGGGTTCAAGCACCCCGCCCTTCACTGGATCCTACAGGGTCTTAAGGCCNA 260
QY 201 TTCCTACGGCCGCTTTCGATGAGGAGCAAGCCCGAGGGGCAAGTTT----- 246
DB 261 CGACTTCAGCTCTGTGTGATGACAGCTTGATCCTGGCAATGCTTTCTTTGCTTGACAA 320
QY 247 -CAAGAGAACCTTGGCAAGCGCACTCGACTTGTGTATG-----CAGTCAAGGTGT 299
DB 321 AGTAGTGGGCTTGGGAAGATTTCTCTGATAACTTAGAGCCCTCTTTATGACATGGC 380
QY 300 CCAGGCGGTGCTTCCCGAGGTGAGGAGTCCCTCAACATCAACGTGTGCGGCGCGCGG 359
DB 381 CCAGGCTAGTGTCTCCATGAATGAGGACTGTCTTACCTTAACTTTCCGCGCCGCTGG 440
QY 360 CACCAAGGGGGCGGCAACCTCCGGTCAATGCTCTGGAATCTTTGGGGGTGGGTTTGAT 419
DB 441 CACCAAGCGCTGATGTAAAGCTCCCGCTCATGTTTGGATTTACGGTGTGCTTTGTGT 500
QY 420 CGGAGCGCCCACTCTTCCCTCCCGCCAGATGTGTCACCAAGAGTGTGCTCATCGGCA 479
DB 501 TGGTCTTCTGCTTCTTACCTTGGTAAACGGCTACGTCAAGGAGAGTGTGGAAATGGGCA 560

QY 480 GCACATCATCCAGTGGCGCTCAACTACCGTGTTCCTCGTGGGGTTCCTTGGCTGTGA 539
DB 561 GCCTGTGTGTTGTTTTCATCAACTACCGTACCGGCCCTATGATTCCTTGGTGGTGA 620
QY 540 TGACATCAAGGCCGAGGGGAGCGCGGCTTGAAGGACCAAGCGTTTGGGCAATGA 599
DB 621 TGCCATCACCGCTGAGGGCAACACCAACGCTGTGTGACACCAAGCGAAGGCTCGA 680
QY 600 GTGGGTGGCAGACAACATTTGCGGGTTCGGCGGCGACCCGACCAAGGTGACTATCTTCG 659
DB 681 GTGGGTGAGCACAACATTTGCGGATCCCGAAGGTCATGATTTTCG 740
QY 660 CGAGTCTCGGGCAGCATGTCCGTGTGTGCCACCTCATCTGGAACGAGCGGACAAAC 719
DB 741 TGAGTCCGCTGTGTCATGAGTGTGCTCACCAGCTTGTGCTACGGTGGTGACAAAC 800
QY 720 GTAACAAGGGCAAGCGGTTTTCGGCGGCGGCAATGAGTCTGAGCCATGGTGC--- 776
DB 801 CTACAACGGAAGCAGCTTTTCCACTCTGCCATTTCTCAGTCTCGGGTCTCTTCTTCT 860
QY 777 -----GTCTGACCCGGTGGACGCGACCTACGGCAACGAGATCTACGACCTCTTTGTCTC 830
DB 861 CTTTGACTCTACTTCTGTGTGTCGAGAGTCCCTACAGAGATTTGCTCAGTATGCCGG 920
QY 831 GAGTCTGTGTCAGCGCGCAGCAAGCTCGCGTGTCTTGGCAGTGCCTTAGCGA 890
DB 921 ATGTGACACCAAGTGCAGTGATATGACACTCTGCGTTGTCTCCGACGAACTCCAGCGA 980
QY 891 CACCTTGTCTGATGC-----CACCAACAACACTCTCGGGTCTTGGGGTACTCTCTCGTT 944
DB 981 TGTCTTGACACAGTGGCAGAACTCGTATGATCTTAAGGACCTGTTTGGTCTGCTCCCTCA 1040
QY 945 GCGGTGTCTTATCTCCGCGCGCGCAGCAAGCAATCAACGATACATGTACAGTT 1004
DB 1041 ATTCTTGATTTGTTCCAGACCGCGCAACATTTATTCGATGCGGCTTATGAGCT 1100
QY 1005 GGTGCGCAACGCAAGTATGCAAGGTTTCCGTGATCATTTGGCGACCAAGACGAGGG 1064
DB 1101 CTACCGCAGCGGTAGATACGCAAGTTTCCCTACATTAATGCAACACGAGGATGAGGG 1160
QY 1065 CACCATCTTGGGCTCTCTTCTTGAAGTACACGAAATGCTAGGCGCGGTACTT 1124
DB 1161 TACTATTCTTGGCCCGTGTCTATTAATGTACCACTACTCCCAATGTTAAGAAGTGGTT 1220
QY 1125 CAAGCAGTCTTTCATCCACGCGCAGCGAGATCGACACCTTGTATGGCGCGTACCC 1184
DB 1221 GAAGTACATTTGTAGCCAGGCTTCTGACGCTTCGCTTGATCGTGTGTTTGTCTACCC 1280
QY 1185 CCAGGACATCACCGAGGTTCTCGGTTCCGACACGGGTGTTCTCAACGCGCTCACCCCGCA 1244
DB 1281 CGGCTCTTGGTGGAGGGTTCAACCATTCGCACTGGTATTTCTTAATGCTCTTACCCCTCA 1340
QY 1245 GTTCAAGAGATCTTGGGCTGTCGGGCACTTGTGATTTCAATCCACGCGCGCTACTT 1304
DB 1341 GTTCAAGCGCATTTGTGCAATTTTCACTGATTTGTGTTTCCAGTCTCCTCGTGTGTTAT 1400
QY 1305 CCTCAACACCTTCCAGGCGCGCAACAGTACTCGTTCTCTTAAGCAGCTCTCT---GG 1361
DB 1401 GCTTAACGCTACCAAGGACGTCACCGCTGGAGTTTACCTTGGCCACCGAGTCCATAACCT 1460
QY 1362 GTTGCAATCATGGGCACCTTCCATGCAACAGCAATTTGTGGCAGGACTACTTCTTGGG 1421
DB 1461 GGTTCATTTTGGGTACTTTCCATGGCAGTATCTCTTTTCAATACTAGTGGACCT 1520
QY 1422 AAGCGGCAAGCTCATCAACAACCGGTTTATCGGTTTCGCCACCGACTTGGACCCCA 1481
DB 1521 TGGGCCATCTTCTGTCTTACCGCGCTACTTTATCTCGTTTGGCAACCAACGACCCCAA 1580
QY 1482 C 1482
DB 1581 C 1581

RESULT 3

US-08-776-210-5
; Sequence 5, Application US/08776210
; Patent No. 5942659
; GENERAL INFORMATION:
; APPLICANT: ALBERT, Gilbert
; APPLICANT: MOULOUNGUI, Zephirin
; APPLICANT: BOUDET, Alain
; TITLE OF INVENTION: PROCESS FOR PRODUCING FATTY ACIDS OR
; TITLE OF INVENTION: DERIVATIVES THEREOF FROM OLEAGINOUS PLANTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,210
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 09272
; FILING DATE: 25-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00957
; FILING DATE: 18-JUL-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: IN 387 - BE 6996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1635 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-776-210-5
Query Match 20.2%; Score 332.2; DB 2; Length 1635;
Best Local Similarity 54.3%; Pred. No. 5.9e-71;
Matches 825; Conservative 0; Mismatches 653; Indels 41; Gaps 6;

QY	39	GGTACCCACCGCAAGCTCGCCAAAGCGGCGACACCATCACCGGTCTCAACGCCATCATCAA	98
DB	3	GGCCCCCGCGGTCTTAATGGCAACGAGGTCACTCTGGTGTCTTGGGGGCAAGGT	62
QY	99	CGAGGGTCTCTGGGATTCCTTTTCCGAGCGCGCGTGGGCAACCTCCGCTTCAAGGA	158
DB	63	TGATACCTTTAAGGGAAATCCATTTGCTGACCTCTGTTGGTGTGCTTGGCGTTCAAGCA	122
QY	159	CCCTGTGCGTACTCTGGTCTGCTCAACGGCCAGAGTTCATCTTTAGGGCCGCTTTG	218
DB	123	CCCCCAGGCTTTTCACTGGATCTTACAGGGTCTTAAGGCCAACGACTTCAGCTCTGCTTG	182
QY	219	CATGACGAGAACCCCGAGGGCACGTTT-----GAAGAGAACCTTTGGCAA	263
DB	183	TATGACGCTTGATCTCTGGCAATGCCATTTCTTGGCTTGACAAAGTCGTGGGCTTGGAAA	242
QY	264	GAGGCACTCGACTTGGTGATG-----CAGTCCAGGTGTTCAGGGGGTCTTCCCA	317
DB	243	GATTTCTTGATACTTATAGAGGCCCTTTTATGACATGGCCCGGAGGTAGTGTCTCCAT	302

QY	318	GAGTGAGACTGCCTCACCATCAACGTGCTGGGCGCGGGCCACCAAGGCGGGCGCCAA	377
DB	303	GAATGAGACTGTCTCTATACCTTAAAGTTTTCGGCCCTGCTGGCACCAAGCCCTGATGCTAA	362
QY	378	CCTCCCGGTCTATGCTCTGGATCTTTGGCGGTGGGTTTGAGATCGGCAGCCGCCCATCTT	437
DB	363	GCTCCCGGTCTATGCTCTGGATCTTTGGCGGTGGGTTTGAGATCGGCAGCCGCCCATCTT	422
QY	438	CCCTCCCGGTCTATGCTCTGGATCTTTGGCGGTGGGTTTGAGATCGGCAGCCGCCCATCTT	497
DB	423	CCCTGGTAAACGCTACGTCAGGAGAGTGTGAAATGGGCCAGCCGCTGTGTGTGTGTTTC	482
QY	498	CGTCAACTACCTGCTGTGCTCTGGGCGGTCTTGGCTGGTGTGATGATCAACAGGCGGAGG	557
DB	483	CATCAACTACCTGCTGTGCTCTGGGCGGTCTTGGCTGGTGTGATGATCAACAGGCGGAGG	542
QY	558	CAGCGGAAACGCGGCTTTGAAGGACACGCTTTGGGCTATGCGTGGTGGGCGAGACAACAT	617
DB	543	TAAACACCAACGCTGTCTGACGACGAGGCAAGGCTCTCGAGTGGGTAGGCGACAACAT	602
QY	618	TGCGGGTTCGCGCGGCGAGCCGAGCAAGGTGACTATCTTTGGCGAGTCTGGGGGAGCAT	677
DB	603	TGCCAACTTTGGTGTGATCCCGACAAGGTCAATGATTTTCGGTGAAGTCCGCTGTGCTCAT	662
QY	678	GTCCGTGTGTGCCACCTCATCTGGAACGAGCGGCGACACAGCTACAGGCGGCAAGCCGTT	737
DB	663	GAGTGTGCTCACCAGCTTTGTCCTACGCTGGTGGTGAACACACTTACAACGGAAGAGCT	722
QY	738	GTTCGCGCGGCGCATCATGAGTCTGGAGCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT	788
DB	723	TTTCCACTCTGCCATCTTCACTCTGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	782
QY	789	GGACGGCACGTACGGCAACGAGATCTACGACTCTTTGTCTCGAGTGTGCTGTGGGAG	848
DB	783	TGGTCCCGAGAGTGCCTACAGCAGATTTGCTCAGTATCCGAGTGTGATGCGAGCGCCAG	842
QY	849	CGCCAGCGACAGCTCGCGTCTGCGCAGTGGCTAGCGACACACTTGTCTGATGCGCAC	908
DB	843	TGACAACTGAACTCTGGCTGTGCTCCGAGCAAGTCCAGCGATGCTTGGCAAGTGCCCA	902
QY	909	CAAC-----AACACTCTCGGTTCTTTGGGTACTCCTCGTGTGGTGTGCTTATCTCC	961
DB	903	GAACTCGTACGATCTCAAGGACCTGTTTGGGCTGCTCTCTCAATTTCTTGGATTTGGTCC	962
QY	962	CGCGCCGCGAGCGCAAGATCAACGATGATGATGATGATGATGATGATGATGATGATGAT	1021
DB	963	C-AGACCCGCGGCAACATTTATCCGATGCGCTTATGAGCTCTACCGCAGCGGTAGAT	1021
QY	1022	ATGCAAGCGTTTCCGCTGATCATTTGGCGACAGAACGAGGCGACCATCTTTGGGCTCT	1081
DB	1022	AGCCAGGTTTCCCTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT	1081
QY	1082	CTTCTTTGAGCGTGAACCAAGTGTCTAGGCGCGGTGCTTACTTCAAGCAGTCTTTTATCC	1141
DB	1082	TTGCTATTATGCTACACAGCTCTCCCATGTTAAGAGTGGTTGAAGTACATTTCTAGCG	1141
QY	1142	AGCCAGCGACGCGGAGATCGACACTTGTATGGGCGGTACCCCGAGGACATCACCGAGG	1201
DB	1142	AGGCTTCTGAGCGCTTTCGCTTGTATGCTGTTTGTGCTCTACCCCGGCTCTTTGGTCCGAGG	1201
QY	1202	GTTCCTCGTCTGACACGCGGTGTTCTCAACGCCCTCACCCCGCAGTTCAAGAGAACTCTCTG	1261
DB	1202	GTGCGCCATTCGCACTGCTGATTTCTTAATGCTCTGACCCCTCAGTTCAAGCGCATGCTG	1261
QY	1262	CGGTCTCGGCGACCTTGCATTCACCGCGCGGCTACTTCTCAACCACTTCCAGG	1321
DB	1262	CAATTTTCACTGATTTTGTGTTTCCAGTCTCTCTCGTGTGTTATGCTTAACGCTACCAAGG	1321
QY	1322	GCGGACCAAGTACTGCTCTCTTAAGCAGCTCTCT-----GGGTGGCAATCATGGCA	1378
DB	1322	ACGTCAACCGTGGACTTACCTTGGCCACCCAGCTCCATAACCTCGTTCCATTTTGGGTA	1381

RESULT 5

US-07-846-181-6
 ; Sequence 6, Application US/07846181
 ; Patent No. 5360732
 ; GENERAL INFORMATION:
 ; APPLICANT: BERKA, RANDY M
 ; APPLICANT: FOWLER, TIMOTHY
 ; APPLICANT: REY, MICHAEL W
 ; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
 ; TITLE OF INVENTION: CATALASE-R
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
 ; STREET: 180 KIMBALL WAY
 ; CITY: SOUTH SAN FRANCISCO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/846,181
 ; FILING DATE: 19920304
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HORN Ms, MARGARET A
 ; REGISTRATION NUMBER: 33401
 ; REFERENCE/DOCKET NUMBER: GC204-US1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-742-7536
 ; TELEFAX: 415-742-7217
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-07-846-181-6

Query Match 9.2%; Score 151.6; DB 1; Length 8533;
 Best Local Similarity 53.5%; Pred. No. 8.5e-27;
 Matches 590; Conservative 0; Mismatches 484; Indels 28; Gaps 12;

QY	322	GAGGACTGCTCACCATCAACGTGGTGGCGCCGCGGACCAAGCGGCGGCCAACCTC	381
DB	12	GAGGATGTCTGAACATGACATTCGGCGCCGAGCAACCCCACTGGCGGCGGAATGC	71
QY	382	CCGGTCATCTCTGGATCTTTGGCGGTGTGAGATCGGCAGGCCCAACCATCTTCCCT	441
DB	72	CCGTGCTGCTCGGATCTTTGGCGGAGCTTTGAACTGGTTCAAAGCCATGATGAC	131
QY	442	CCGCCCCAGATGGTCACCAAGAGTGTCTCATGGGCAAGCAATCATCCACGTGGCCGTC	501
DB	132	GGCAACCAACGATGGTATCATCGTCGATAGACAAGAATATGCCATCTGCTGTGTAGCGATG	191
QY	502	AACTACCGTGTGCTCGTGGGGTCTTGGTGGTGTGATGACATCAAGCCGAGGCGAGC	561
DB	192	AACTATCGGTAGGGGGCTTCGGGTTCTGCCCGAAGAGGATTTCTGGAGGACGGTCC	251
QY	562	GGGAACCGCGGCTTGAAGACCAAGCGTTTGGGCATGTCAGTGGGTGGCGAGACAACATGCC	621
DB	252	GCCAACTTAGG--TCTTTGACCAAGCCTTGCCC---TAGTGGGTGGCGACAACATCGAG	306
QY	622	GGGTTGGGCGGACCCGAGCAAGGTGATCTTTGGCGAGTCTGGCGGCGAGCATGCC	681
DB	307	GGCTTTGGTGGAGACAGA--CAAGGTGCAATCTGGGGAGATACGACGAGGGGCTATTCT	365

QY	682	GTGTTGTGCCACCTCATCTGGAAACGACGGCGACACACGTAACAAGGGCAAGCCGTGTTC	741
DB	366	GTCTTTGATCAGATGATCT--GTACACGGAACATCGCTTACAGGACAAGCCCTTGTTT	423
QY	742	CGCGCGGCATCATGACAGTCTGGAGCCATGGTGCCGTCTGACCCCGGTGGACGGCACGTAC	801
DB	424	CG--GGAGCCATCATGGAATCCGGT--ATGTGTTCCGCGAGACCCCTGTCGAGGGGTCAAGG	481
QY	802	GGCAACGAGATCTACGACCTCTTTGTCTCGAGTGTGGTGTGGCAGCGCCGACGACAAG	861
DB	482	GATCAGCAAGTATATGATGCGGTTGTGACTCTGCAAGCTGTCTCTCTTCCAACGACACC	541
QY	862	CTCGCGTCTTGGCGAGTCTAGCGACACCTTGTCTCGATGCCACCAACACACTCTCT	921
DB	542	CTGGCTTGTCTGCGTAGCTAGACTACACCGACTATCTCAATGCGGCAAACTCTGTCGCGG	601
QY	922	GGGTTCTTGGCGTACTCTCGTTGGGTGTGTTATCTCCCGCGGCCCGACGCAAGAAC	981
DB	602	GGATCTAGTTATCACCG--TGGCGCTATCATATGTCCCTCGACACGAGCGGACGCA	658
QY	982	ATCACCGATGATGATACAAGTTGGTGGCGGACGCAAGATGCAAGGTTTCCCGTGTATC	1041
DB	659	TTTGTGCGGCTC--GCCAGATTTTGGGTAAAGCAGGGAAGTATGCGCGGTCCCATTTCTC	717
QY	1042	ATTGCGGACCAAGACGAGGCGACCATCTTTGGGCTCTCTTCTTTGAACTGTGACACG	1101
DB	718	GTGGCGGACCAAGAGGATGAGGGGACC--TTGTTGCGCTTGTGTTTCAAGTCTTACGACGATC	776
QY	1102	AATGCTCAGGCGCGTCTTACTTCAAGCAGTCTTTTCAAGCCGCGGACGCGGAGATC	1161
DB	777	GACGAGGTAGTCGACTATCTGGGCACCTACTTCTTCTATGACGCTAGCCAGGACGCTT	836
QY	1162	GACACCTTGTATGGCGGCGTACCCCGAGGACATCACCCAGGTTTCTCGTTGACACGGGT	1221
DB	837	GAAGAATTTAGTGGCCCTGTACCCAGACACACCATATATGGGTCTCTCCCTTCAGGACGGC	896
QY	1222	GTCTCTCAAGCGCTTCAACCCCGCAGTTCAAGAGAATCTCTGGGTCTCGGCGACCTTCA	1281
DB	897	AGGC--CAACAACTGGTATCCGCAATTTAAGCATTTGGCGCCCATTTCTCGGCACTTGTTC	955
QY	1282	TTTCATCCACGCGCGCGCTACTTTC-----CTCAACCACTTCCAGGCGCGCACCA	1330
DB	956	TTTCAACATTTACCGCGCGCATTTCTGTCTATATGACAGGAGCTCTCCCTGACCTCCCGA	1015
QY	1331	AGTACTGTTCTCTTAAGCAGCTCTCTGGTTGCGCAATCATGGGACCTTCCATGCA	1390
DB	1016	AATGTCGTACTCTGGCGACCTATGACTAT--GGCAGCCAATTTGGGGACCTTTCATGGAA	1074
QY	1391	ACGACATTTGTGGCAGGACTA 1412	
DB	1075	GTGACCTCTGAGGTGTTCTA 1096	

RESULT 6

US-07-845-989-6
 ; Sequence 6, Application US/07845989
 ; Patent No. 5360901
 ; GENERAL INFORMATION:
 ; APPLICANT: BERKA, RANDY M
 ; APPLICANT: FOWLER, TIMOTHY
 ; APPLICANT: REY, MICHAEL W
 ; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
 ; TITLE OF INVENTION: CATALASE-R
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
 ; STREET: 180 KIMBALL WAY
 ; CITY: SOUTH SAN FRANCISCO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk


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;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1842
; US-07-732-962A-1

Query Match
Best Local Similarity 4.5%; Score 74.4; DB 1; Length 1845;
Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;

QY 290 CCAAGGTGTTCCAGGCGGTGCTTCCAGAGTGAGGACTGCTCACCATCAACGTGGTGC 349
Db |||||
QY 341 CCGAGATGGAACCCCAACCTGAGCTGAGCGAGGACTGCTGTACCTCAAC---GTGT 397
Db |||||
QY 350 GGCCTGGGCAACCAAGGGGGGCGCAACCTCCGGTCAATGCTCTGGATCTTTGGCGGTG 409
Db |||||
QY 398 GGACACCATACCCCGGGCTTACATCCCAACCTCCCTCGTCTGGATCTATGGGGTG 457
QY 410 GGTGTTGAGTCCAGGCGGCTTCCCTTGGACGTGTACGATGCGCGCTTC-----TTGG 469
Db |||||
QY 458 GCTTCTACAGTGGGCTTCTCTTGGACGTGTACGATGCGCGCTTC-----TTGG 508
QY 470 TCATGGGCAAGCACAATCAAGGCGGAGCGCGGCTTGAAGGACCAAGCGCTT 529
Db |||||
QY 509 TACAGGCGGAGAGGACTGTGCTGGTGTCCATGAACCTACCGGTGGGAGCTTTGGCTTCC 568
QY 530 TGGCTGGTGTATCATCAAGGCGGAGCGCGGCTTGAAGGACCAAGCGCTT 589
Db |||||
QY 569 TGGCCCTGCCGGGAGC---CGAGAGGCGCCGGCAATGTGGTCTCTGGATCAGAGGC 625
QY 590 TGGGATGAGTGGGTGGGAGACACATGTCGGGTTCGGCGGCGACCGGAGCAAGTGA 649
Db |||||
QY 626 TGGCCCTGAGTGGGTGCAAGGAGACGTGGCGAGCTTGGGGGTGACCGGACATCAGTGA 685
QY 650 CTATCTTTGGCGAGTGTGGGCGAGCATGTCCGCTTGTGTCACCTCATCTGGAACGAGC 709
Db |||||
QY 686 CGCTGTTTGGGAGAGCGCGGAGCGCTTGGTGGGATGATGATGAGGCTCGT 745
QY 710 GGCACACACGTACAAAGGCAAGCGTGTTCGGCGGGGCAATGATGATGTGAGGCA 769
Db |||||
QY 746 GCGGGGCGCTGTTCACAGGGCGCTGCTGCAGAGCGGTGCCCAATGAGACCTGGGCA 805
QY 770 TGGTCCGCTCTACCGCGTGGAGCGCATGTCCGCTTGTGTCACCTCATCTGGAACGAGC 829
Db |||||
QY 806 CGGTGGGCAATGGAGAGGCGCTGAGG---GCCAGCAGCTGGCCACCTTTGGGCT 862
QY 830 CGAGTGTCTGGCTGTGGCAGCGCCAGCGCAAGCTCGCGTGTGTCGCGAGTGGCTTAGCG 889
Db |||||
QY 863 GTCTCCAGGCGGCATGTTGGGAATGACACAGAGCTGGTAGCTGCTCGGACACGAC 922
QY 890 ACACCTTGTCTGATGCCACCAACACATCTCTGGGTCTTGGCGGTACTCTCTGGTGGGT 949
Db |||||
QY 923 CAGCGCAGGTCTCTGTGAACCAAGAAATGGCAGCTGCTGCTCAAGAAAGCGCTTTCGGT 982
QY 950 TGTCTTATCTCCGGCGCGGCGGAGCAAGACATCAGGATGACATGTACAGTTGGTGC 1009
Db |||||
QY 983 TCTCTCTGCTGTGTGTAGATGGAGACTTCTCAGTGACACCCAGAGGCGCTTCATCA 1042
QY 1010 GCGAGGCAAGTATGCAAGCGTTCCTCGTATCATTTGGGCGACAGAAACGACGAGGCGCA 1069
Db |||||
QY 1043 AGCGGGAGACTTCCACGCGCTGACAGTGTCTGTTGGTGTGGTGAAGATGAGGCTCGT 1102
QY 1070 TCTTTGGGCTCT 1081
Db |||||
QY 1103 ATTTCCTGGTTT 1114
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RESULT 12

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PCT-US92-06106-1
; Sequence 1, Application PC/TUS9206106
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
```

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; TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
; MOLECULE TYPE: ACETYLCHOLINESTERASE AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; STREET: John P. White, Esq.
; CITY: 30 Rockefeller Plaza
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06106
; FILING DATE: 19920722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1845 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1842
; PCT-US92-06106-1
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Query Match 4.5%; Score 74.4; DB 5; Length 1845;
Best Local Similarity 47.1%; Pred. No. 2.7e-08;
Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;
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QY 290 CCAAGGTGTTCCAGGCGGTGCTTCCAGAGTGAGGACTGCTCACCATCAACGTGGTGC 349
Db |||||
QY 341 CCGAGATGGAACCCCAACCTGAGCTGAGCGAGGACTGCTGTACCTCAAC---GTGT 397
Db |||||
QY 350 GGCCTGGGCAACCAAGGCGGCGCGCAACCTCCCGGTCAATGCTCTGGATCTTTGGCGGTG 409
Db |||||
QY 398 GGACACCATACCCCGGGCTTACATCCCAACCTCCCTCGTCTGGATCTATGGGGTG 457
QY 410 GGTGTTGAGATCGGAGCGGCGGCAACCTTTCCTCCCGCCAGATGGTCAACAGAGTGTGC 469
Db |||||
QY 458 GCTTCTACAGTGGGCGCTTCTCTTGGACGTGTACGATGCGCGCTTC-----TTGG 508
QY 470 TCATGGGCAAGCACAATCAAGGCGGAGCGCGGCTTGAAGGACCAAGCGCTT 529
Db |||||
QY 509 TACAGGCGGAGAGGACTGTGCTGGTGTCCATGAACCTACCGGTGGGAGCTTTGGCTTCC 568
QY 530 TGGCTGGTGTATCATCAAGGCGGAGCGCGGCTTGAAGGACCAAGCGCTT 589
Db |||||
QY 569 TGGCCCTGCCGGGAGC---CGAGAGGCGCCGGCAATGTGGTCTCTGGATCAGAGGC 625
QY 590 TGGGATGAGTGGGTGGGAGACCAATGTCGGGTTCGGCGGCGACCGGAGCAAGTGA 649
Db |||||
QY 626 TGGCCCTGAGTGGGTGCAAGGAGACGTGGCGAGCTTGGGGGTGACCGGACATCAGTGA 685
QY 650 CTATCTTTGGCGAGTGTGGGCGAGCATGTCCGCTTGTGTCACCTCATCTGGAACGAGC 709
Db |||||
QY 686 CGCTGTTTGGGAGAGCGCGGAGCGCTTGGTGGGATGATGATGAGGCTCGT 745
QY 710 GCGACACACATGACAAAGGCGCAAGCGTGTTCGGCGGGGCAATGATGATGTGAGGCA 769
Db |||||
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Db 746 GCGGGGCTGTTCACAGGGCGTGTCTGACAGCGGTGCCCCCAATGACACCTTGGGCCA 805
Qy 770 TGGTGGCGTGTACCGCGGTGGACGGCAGCTACGGCAACGAGATCTACGACCTTTTGTCT 829
Db 806 CGGTGGGATGGAGAGGCCCTGCGAGG---GCCACGAGCTGGCCCACTTGTGGGCT 862
Qy 830 CGAGTGTGGTGTGGCAGCGCCAGCACAAGCTCGCGTCTTGGCAGTGGGTCTAGCG 889
Db 863 GTCCTCAGGCGGCACTGGTGGGAATGACACAGAGCTGGTAGCCTTCGGACACGAC 922
Qy 890 ACACCTTGTCTGATGCCACAACAACACTCTCTGGGTTCTTGGGTAATCTCTGTTGGGT 949
Db 923 CAGCGCAGTCTCTGTGTGAACCAAGATGGCAGCTGCTCTCAAGAAAGCTCTTCGGGT 982
Qy 950 TGTCTTATCTCCCGCGGCCGCGGCAAGAAATACACCGATGACATGTACAAGTTGGTGC 1009
Db 983 TCTCTTCTGCTGTGTAGATGGAGACTTCTCAGTGACACCCAGAGGCCCTCATCA 1042
Qy 1010 GCGACGGCAAGTATGCAAGCGTTTCCCGTGTATCATTTGGCGACCAAGACGAGGGCACCA 1069
Db 1043 ACGCGGAGACTTCCACGGCGCTGCAGTGTCTGTGGTGTGGTGAAGATGAGGCTCGT 1102
Qy 1070 TCTTTGGGCTCT 1081
Db 1103 ATTTTCTGTTT 1114

RESULT 13
US-09-949-016-1192
; Sequence 1192, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1192
; LENGTH: 2158
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1192

Query Match 4.5%; Score 74.4; DB 4; Length 2158;
Best Local Similarity 47.1%; Pred. No. 2.9e-08;
Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;
Qy 290 CCAAGGTGTTCCAGCGGTGCTTCCCGAGTGAGGACTGCTCACCATCAACGTGGTGC 349
Db 435 CCGAGATGGAAACCCCAACCGTGAGCTGCGAGGAGTGCCTGTACCTCAAC---GTGT 491
Qy 350 GCGCGCGCGGCACCAAGGGCGGCGCAACCTCCCGTCAATGCTCTGGATCTTTGGCGGTG 409
Db 492 GGACACCATACCCCGGCTTACATCCCGCACCCCTGTCTCTGTCTGGATCTATGGGGTG 551
Qy 410 GGTGTTGAGATCGGCAGCCCAACCATTTCTCCCTCCCGCCAGATGGTCAACAGAGTGTGC 469
Db 552 GCTTCTACAGTGGGGCTCTCTCTTGGACGTGTACGATGGCGCGCTTC-----TTGG 602
Qy 470 TCATGGGCAAGCACATCATCCAGTGGCGGTCACTACCGTGTTCGCTGCGGGGTTCT 529
Db 603 TACAGGCCGAGAGGACTGTGTGTTGTTCCATGAATACCGGTGGGAGCTTTTGGCTTCC 662
Qy 530 TGGCTGGTGTATGATCAAGGCGGAGGCGAGCGGGAACGCCGGCTTTGAAGGACACGCTT 589
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Db 663 TGGCCCTGCGGGGAGC---CGAGAGGCCCGGCAATGTGGGTCTCTTGATCAGAGGC 719
Qy 590 TGGGATGAGTGGGTGGCAGACAATTCGCCGGGTTTCGGCGGCGACCCGAGCAAGTGA 649
Db 720 TGGCCCTGCAAGTGGGTGCGAGAGAACGTGGCAGCCTTCGGGGGTGACCCGACATCAGTGA 779
Qy 650 CTATCTTTGGGAGTCTCGCGGCACATGTCCGTGTTGTGCCACCTCATCTGGAACGACG 709
Db 780 CGCTGTTTGGGAGAGCGCGGAGCCGCTCGGTGGGATGACCTGTCTCCCGCCCA 839
Qy 710 GCGACAACACGTACAAAGGCGAAGCGTTTTCGCCGCGGCGCATCATGCAAGTCTGGAGCCA 769
Db 840 GCGGGGCTGTTCACAGGGCGGTGTCAGAGCGGTGCCCCCAATGGAACCTGGGCCA 899
Qy 770 TGGTGGCTGTGACCCCGTGGACGACGTAGCGGAACAGATCTACGACCTCTTTGTCT 829
Db 900 CGGTGGGATGGGAGAGGCCCTGTCGAGG---GCCACGAGCTGGCCCACTTGTGGGT 956
Qy 830 CGAGTGTGGCTGTGGCAGCGCCAGCAAGCTCGCGTGTTCGCGAGTGGCTAGCG 889
Db 957 GTCCTCCAGGCGGCACTGTGTGGATGACACAGCTGTAGCTGCTTCGACACGAC 1016
Qy 890 ACACCTTGTCTGATGCCACCAACACTCTCTGGGTTCCTGGCGTACTCTCTGTCGGT 949
Db 1017 CAGCGCAGGTCTCTGTGAACCAACGAGTGCACGTCTGCTCAAGAAAGCGTCTTCGGT 1076
Qy 950 TGTCTTATCTCCCGCGGCCGCGCAGCAAGACATCACCAGTACATGATGATGATGATG 1009
Db 1077 TCTCTCTGCTGTGTAGATGGAGACTTCTCAGTGACACCCAGAGGCCCTCATCA 1136
Qy 1010 GCGACGGCAAGTATGCAAGCGTTCCCGTGTATCATTTGGCGACCAAGACGAGGCCACCA 1069
Db 1137 ACGCGGAGACTTCCACGGCTGCGGTGTGGTGTGGTGTGGTGAAGATGAGGCTCTGT 1196
Qy 1070 TCTTTGGGCTCT 1081
Db 1197 ATTTTCTGTTT 1208

RESULT 14
US-09-949-016-1193
; Sequence 1193, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1193
; LENGTH: 2158
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1193

Query Match 4.5%; Score 74.4; DB 4; Length 2158;
Best Local Similarity 47.1%; Pred. No. 2.9e-08;
Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;
Qy 290 CCAAGGTGTTCCAGCGGTGCTTCCCGAGTGAGGACTGCTCACCATCAACGTGGTGC 349
Db 435 CCGAGATGGAAACCCCAACCGTGAGCTGCGAGGAGTGCCTGTACCTCAAC---GTGT 491
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350 GGCCGCCGCGCCACCAAGCGCGCGCAACCTCCCGTCACTGCTGATCTTTGGCGGTG 409
492 GGACACCATACCCCGGCTCATCCCCACCCCTGCTCTGATCTATGGGGTG 551
410 GGTGTTAGATCGGACGCCACCATCTTCCCTCCCGCCAGATGTCACCAAGATGTGC 469
552 GCTTCTACAGTGGGGCTCTCTTGGACGTGACGATGGCGGCTTC-----TTGG 602
470 TCATGGGCAAGCACATCATCTACGTGGCGGCTCACTACCGTGTGCTGCGGGGTCT 529
603 TACAGCCGAGAGGACTGTGCTGGTGTCCATGAATACCGGTGGGAGCTTTGGCTTCC 662
530 TGGCTGCTCATGACATCAAGGCGGAGGCGAGGCGCGGAAACCGCGCTTTGAAGGACCAAGCTT 589
663 TGGCCCTGCGGGGAGC----CGAGAGGCCCGGGGATGTGGGTCTCTGGATCAGAGC 719
590 TGGGATGTCAGTGGGTGGGAGCAACATTTGCCGGGTTCGGCGGCGACCCGAGCAAGGTGA 649
720 TGGCCCTGCACTGGGTGGGAGGAGACGTGGCAGCCTTCGGGGGTGACCCGACATCAGTGA 779
650 CTATCTTTGGCAGTCTGGGCGAGCATGTCGTGTTGTGTCACCTCATCTGGAAGAGG 709
780 CCGTGTGTTGGGAGAGCGCGGAGCGCGCTCGGTGGGATGCACCTGTCTCCCGCCCA 839
710 GCGACAAACGCTACAGGCGCAAGCCGTTGTTCCGCGCGGCGCATGTCAGTCTGGAGCCA 769
840 GCGGGGCTGTTTCACAGGCGGCTGCTGACAGCGGTGCCCCCAATGGACCTGGGCCA 899
770 TGGTGGCTGTACCCCGGTGAGCGGACGTCAGGCAACGAGATCTACGACCTCTTTGTCT 829
900 CGGTGGGATGGAGAGGCGCGTGCAGG---GCCACGCGAGCTGGCCCAACCTTGTGGGT 956
830 CAGTGTGCTGTGGCAGCGGCGGAGCAAGCTCGGTGTTGGCGAGTGTCTAGG 889
957 GTCTCCAGGCGGCACTGGTGGGAATGACACAGAGCTGGTACCTGCTTCGACACGAC 1016
890 ACACCTTGTCTGATGCCACCAACACACTCTCTGGGTTCCTGCGTACTCTCTGTCGGT 949
1017 CAGCGGAGTCTGTGTAACACAGATGGCAGCTGCTGCTCAAGAGCGTCTTCCGGT 1076
950 TGTCTTATCTCCCGGCGCGCGGCAAGAACATCACCAGATGACATGACAGTGTGGTGC 1009
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1010 GCGAGCGCAAGTATGCAAGCTTCCGCTGATCATTTGGGACAGACAGAGGCGACCA 1069
1137 ACGCGGAGACTTCCACGCGCTGCAGGTGCTGGTGGTGTGGTGAAGGATGAGGCTCT 1196
1070 TCTTTGGGCTCT 1081
1197 ATTTCGTGTTT 1208

RESULT 15
US-08-318-826A-5
; Sequence 5, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,826A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2391.00001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2256 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: /note= "Splice variant: Exons 1, 2,
OTHER INFORMATION: 3, 4 and 6"
US-08-318-826A-5
Query Match 4.5%; Score 74.4; DB 2; Length 2256;
Best Local Similarity 47.1%; Pred. No. 2.9e-08;
Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;
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DB 557 GGACACCATACCCCGGCTTACATCCCGCACCCCTGCTCTGTGATCTATGGGGGTG 616
QY 410 GGTTTGATCGGAGCGGCCACCATCTTCCCTCCCGCCAGATGCTCACCAGAGTGTGC 469
DB 617 GCTTCTACAGTGGGGCTCTCTCTTGGACGTGTAGATGGCGCGCTC-----TTGG 667
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QY 530 TGGTGGTGTGATGACATCAAGGCGGAGGAGCGGGAAACGCGGGCTTGAAGGACCAAGCTT 589
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Qy 950 TGTCTTATCTCCGGCGCGCGGACGGCAAGAACATCACCGATGACATGTACAAGTTGGTGC 1009
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Job time : 377 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2005, 00:44:42 ; Search time 1746 Seconds
(without alignments)
6284.070 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7400704 seqs, 3343079526 residues

Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	77.3	1532	10	US-09-943-857-3
2	984.8	60.0	1541	10	US-09-943-857-7
3	984.4	60.0	1548	10	US-09-943-857-5
4	895	54.5	1511	10	US-09-943-857-9
5	888	54.1	1650	24	US-11-061-894-1
6	888	54.1	1650	24	US-11-061-233-1
7	778.4	47.4	1469	10	US-09-943-857-1

8	354.2	21.6	1687	17	US-10-369-493-27923	Sequence 27923, A
9	119.6	7.3	1716	9	US-09-801-852A-1	Sequence 1, Appli
10	103.8	6.3	1272	17	US-10-369-493-41665	Sequence 41665, A
11	98.4	6.0	1419	17	US-10-369-493-34501	Sequence 34501, A
12	74.4	4.5	1725	9	US-09-810-861B-5	Sequence 5, Appli
13	74.4	4.5	1725	22	US-10-792-491-5	Sequence 5, Appli
14	74.4	4.5	2509	21	US-10-887-553A-108	Sequence 108, App
15	74.4	4.5	5767	9	US-09-810-861B-3	Sequence 3, Appli
16	74.4	4.5	5767	22	US-10-792-491-3	Sequence 3, Appli
17	74.4	4.5	14446	9	US-09-810-861B-4	Sequence 4, Appli
18	74.4	4.5	14446	22	US-10-792-491-4	Sequence 4, Appli
19	73.6	4.5	2312	17	US-10-264-049-858	Sequence 858, App
20	73.6	4.5	2350	21	US-10-741-600-401	Sequence 401, App
21	73.6	4.5	2428	9	US-09-969-347-220	Sequence 220, App
22	73.6	4.5	2428	10	US-09-418-176-1	Sequence 1, Appli
23	73.6	4.5	2428	21	US-10-843-641A-8349	Sequence 8349, Ap
24	72	4.4	2734	20	US-10-781-866-5	Sequence 5, Appli
25	72	4.4	2781	20	US-10-781-866-6	Sequence 6, Appli
26	72	4.4	3004	21	US-09-873-367C-446	Sequence 446, App
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28	70.2	4.3	2191	9	US-09-880-107-3854	Sequence 3854, Ap
29	70.2	4.3	2191	9	US-09-954-531-1038	Sequence 1038, Ap
30	70.2	4.3	2191	10	US-09-873-367C-828	Sequence 828, App
31	70.2	4.3	2191	10	US-09-873-367C-829	Sequence 829, App
32	70.2	4.3	2191	20	US-10-858-271-27	Sequence 27, Appl
33	70.2	4.3	2191	21	US-10-843-641A-828	Sequence 828, App
34	70.2	4.3	2191	21	US-10-843-641A-829	Sequence 829, App
35	70.2	4.3	2191	21	US-10-843-641A-2105	Sequence 2105, Ap
36	70.2	4.3	2202	22	US-10-450-763-10284	Sequence 10284, A
37	70.2	4.3	2484	9	US-09-925-298-271	Sequence 271, App
38	70.2	4.3	2484	14	US-10-102-806-271	Sequence 271, App
39	69.8	4.3	2092	17	US-10-104-047-249	Sequence 249, App
40	69	4.2	1728	18	US-10-451-168-40	Sequence 40, Appl
41	69	4.2	1728	22	US-10-980-387-40	Sequence 40, Appl
42	69	4.2	1746	13	US-10-023-515-3	Sequence 3, Appli
43	69	4.2	1746	18	US-10-114-270-195	Sequence 195, App
44	69	4.2	1746	18	US-10-674-636-3	Sequence 3, Appli
45	69	4.2	1746	18	US-10-451-168-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-943-857-3
; Sequence 3, Application US/09943857
; Publication No. US20030124701A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Jei-Fu
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Jye
; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943.857
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Candida rugosa
US-09-943-857-3

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Best Local Similarity	94.5%	Pred. No. 0;		
Matches 1505;	Conservative	0;	Mismatches 25;	Indels 62;
Gaps	16;			
Qy	43	CCCCCGCCAGCTCGCCAGCGGACACCATCACCGGTCTCAACGCATCATCAACGAG	102	
Db	2	CCCCCGCCAGCTCGCCAGCGGACACCATCACCGGTCTCAACGCATCATCAACGAG	61	
Qy	103	CGCTTCCTCGCATTCCTCTTCCGAGCCGCGGTGGCAACCTCCGCTTCAAGGACCT	162	

Db 62 GCGTTCTCGGATTCCTTTGCGGAGCCGCGTGGCAACCTCGCGTTCAAGGACCT 121
 Qy 163 GTGCGGTACTCTGGCTCGCTCAACGGCAGAGATTCACTTCTTAAGGCCCGTCTTGCAATG 222
 Db 122 GTGCGGTACTCTGGCTCGCTCAACGGCAGAGATTCACTTCTTAAGGCCCGTCTTGCAATG 174
 Qy 223 CAGCAGAAACCCGAGGGCAGCTTTGAAGAGAACTTTGGCAAGACGCACTCGACTTTGGTG 282
 Db 175 CAGCAGAAACCCGAGGGCAGCTTTGAAGAGAACTTTGGCAAGACGCACTCGACTTTGGTG 234
 Qy 283 ATGCAATCAAGGTGTTCAAGCGGTGCTTCCCGAGGTGAGGACTGCTCAACCATCAAC 342
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 Qy 343 GTGGTCCGCGCGCGGGCAGCAAGCGGGCGGCAACCTCCCGGTCAATGCTCTGGATCTTT 402
 Db 295 GTGGTCCGCGCGCGGGCAGCAAGCGGGCGGCAACCTCCCGGTCAATGCTCTGGATCTTT 354
 Qy 403 GCGGGTGGGTGTTGAGATCGGAGCCCAACATCTTCCCTCCCGCCAGATGTCACCAAG 462
 Db 355 GCGGGTGGGTGTTGAGATCGGAGCCCAACATCTTCCCTCCCGCCAGATGTCACCAAG 414
 Qy 463 AGTGTGCTCATGGGCAAGCAGATCATCAAGCGGTGCGGTCAACTACCGGTGCTCGTGG 522
 Db 415 AGTGTGCTCATGGGCAAGC- CATCATCAAGGTGCGGTCAACTACCGGTGCTCGTGG 473
 Qy 523 GGGTCTTGGCTGGTATGACATCAAGCGCGGAGGGGAGCGGAAACGCGGCTTGAAGAC 582
 Db 474 GGGTCTTGGCTGGTATGACATCAAGCGCGGAGGGGAGCGGAAACGCGGCTTGAAGAC 533
 Qy 583 CAGCGTTTGGGATGAGTGGGTGGCAGACATTTGCGGGTTCGGGGCGGACCCGAGC 642
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 Qy 643 AAGGTGACTATCTTTGGCGAGTCTGCGGCGAGCATGTCCGTGTTGTGCCACCTCATCTGG 702
 Db 594 AAGGTGAC-ATCTTTGGCGAG--GCGGGCAGCATGTCGTGTTGTGCCACCTCATCTGG 649
 Qy 703 AACGAGGGCAGCAACACGTTCAAGGGCAAGCGTGTTCGCGGGCGGCAATCATGAGTCT 762
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 Qy 763 GGAGCATGCTGTCGCTGACCCGGTGGAGCGGACGTCAGCGCAACGAGATCTACGACCTC 822
 Db 707 GGAGCATGCTGTCGCTGACCCGGTGGAGCGGACGTCAGCGCAACGAGATCTACGACCTC 763
 Qy 823 TTTGTCTGAGTGTGCTGTGGCAGCGCGCAGCGCAAGCTCGCGTGTTCGCGAGTGG 882
 Db 764 TTTGTCTGAGTGTGCTGTGGCAGCGCGCAGCGCAAGCTCGCGTGTTCGCGAGTGG 823
 Qy 883 TCTAGGACACCTTGTGATGCCACCAACACATCTCTGGGTCTTGGCGTACTCTCTGG 942
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 Qy 943 TTTGGGTGCTCTATCTCCCGCGGCGGAGCGGCAAGACATCACGATGACATGTACAA 1002
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 Qy 1363 TTGCAATCATGGGCACTTCCATGCCAACGACATTTGTGTGGCAGGACTACTTTTGGGA 1422
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 Db 1326 AGCGCAGCGTCACTACAAACGCGTTTATCGGTTTGCACCGACTTGGACCCCAAC 1385
 Qy 1483 ACCGCGGGTGTGTGGTGAACCTGGCCCAAGTACACGAGCTCTCAGTCTGGCAACAC 1542
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 Db 1440 TTGATGATGATCAACGCTTGGGCTTTGACACCGCAAGGACAACTTCGCAACCGCTGGC 1499
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 Db 1500 TACGACGCTTGTGATGACCAACCGCTCTCTTTGT 1531

RESULT 2

US-09-943-857-7
 ; Sequence 7, Application US/09943857
 ; Publication No. US20030124701A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shaw, Jei-Fu
 ; APPLICANT: Lee, Guan-Chiun
 ; APPLICANT: Tang, Shye-Jye
 ; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
 ; FILE REFERENCE: 08919-066001
 ; CURRENT APPLICATION NUMBER: US/09/943.857
 ; CURRENT FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 1541
 ; TYPE: DNA
 ; ORGANISM: Candida rugosa
 US-09-943-857-7

Query Match 60.0%; Score 984.8; DB 10; Length 1541;
 Best Local Similarity 83.2%; Pred. No. 2.1e-268;
 Matches 1327; Conservative 0; Mismatches 212; Indels 55; Gaps 16;

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 Qy 104 CGTTCTCTCGGCAATTCCTTTTCCGAGCGCGCGTGGGCAACCTCCGCTTCAAGGACCCCTG 163
 Db 62 CGTTCTCTCGGCAATTCCTTTTCCGAGCGCGCGTGGGCAACCTCCGCTTCAAGGACCCCTG 121
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 Db 122 TCCGCTACTCTGCTCGCTCAACGCGCAGAGTTCATCTTCTACGCGCGCTTTCGATGC 178
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 Qy 284 TGCAGTCAAGGTGTTCCAGCGGTGCTTCCCAAGAGTGGAGTGTGCTCAACATCAACG 343
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QY 523 GGGTTCTTGGCTGATGACATCAAGCCGAGGGCAGCGGAAACGCGCGTTGAAGGAC 582
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QY 763 GAGGCAATGTCGCTGACCCGGTGGACCGGACGTCAGGCAACGAGATCTACGACCTC 822
Db 707 GGGGCCATGGTGCG - GGACCCGGTGGATGGGCCCTACGGCAGCGAGATCTACGACCA 764
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QY 1003 TTGGTCGGGACGGCAAGTATGCAAGCTTCCGGTATCATTTGGCGACAGAACGAG 1062
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Db 1344 CACAGCAGCGCGGTGTACAAACAGGTTTATTTGGCTTTTGGCTTTCACGACCTTCAGCCGGAAC 1403
QY 1483 ACCGGGGTGTGTGGTGAATGGGCCAAGTACACGACAGTCTCAGTCTGGCAACCAAC 1542
Db 1404 AAGGCCGGTGTGTGTGAATGGGCCAAGTACACCGAGC - ---- CAGGGCAACCAAC 1457
QY 1543 TTGTGATGATCAACGCCCTTGGCTTGTATACCGGCAAGGACAACTTCGCGACCGCTGGC 1602
Db 1458 TTGTGATGATCAACGCCCTTGGCTTGTATACCGGCAAGGACAACTTCGCGACCGCTGGC 1517
QY 1603 TACGACCGCTTGTATGACCAACCCGCTCTT 1630

Db 1518 TACGACGGGTGTTTACCAACCCGTTTT 1545

RESULT 4

US-09-943-857-9
; Sequence 9, Application US/09943857
; Publication No. US20030124701A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Jei-Fu
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Jye
; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943,857
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1511
; TYPE: DNA
; ORGANISM: Candida rugosa
US-09-943-857-9

Query Match 54.5%; Score 895; DB 10; Length 1511;
Best Local Similarity 83.0%; Pred. No. 5.7e-243;
Matches 1321; Conservative 0; Mismatches 185; Indels 85; Gaps 23;

QY 44 CCACGCCCAAGCTCGCCAAACGCGCAGCACCATCACCGGTCTCAACGCCATCATCAACGAGG 103
Db 2 CCCACGCCACGCTCGCCAAACGCGCAGCACCATCACCGGTCTCAACGCCATCATCAACGAGG 61
QY 104 GGTTCCTCGGCATTTCCCTTTGCGAGCGCGGTGGGCAACCTCCGCTTCAAGGACCCCTG 163
Db 62 GGTTCCTCGGCATTTCCCTTTGCGAGCGCGGTGGGCAACCTCCGCTTCAAGGACCCCG 121
QY 164 TGCGGTACTCTGGCTCGCTCAACGCCAGAGTTTCACTTCTTACGCCCGCTCTTCATGC 223
Db 122 TGCGGTACTCTGGCTCGCTCGATGGCCAGAGTTTCACTACGGCC - - - - - CGTGCAATGC 174
QY 224 AGCAAGAACCCCGAGGCGCACGTTTGAAGAGAACTTTGGCAAGACGCGACTCGACTTGGTGA 283
Db 175 AGCAAGAACCCCGAGGCGCACCTTACGAGGAGAACTTCCCAAGGACGCGCTCGACTTGGTGA 234
QY 284 TGCAAGTCAAGGTGTTCAGCGGTGCTTCCCGAGAGTGAGACTGCGCTCACCATCAAG 343
Db 235 TGCAAGTCAAGGTGTTCAGCGGTG - - - - - CCGAGCGAGGACTGTCTCACCATCAAG 288
QY 344 TGGTSCGCGCGCGGCGCACCAAGCGGCGGCGCAACCTCCCGTCACTCTGGATCTTTG 403
Db 289 TGGTSCGCGCGCGGCGCACCAAGCGGCGGTCGCACTCCCGGTGATCTCTGGATCTTTG 348
QY 404 GCGGTGGGTTTGAGATCGGCGACCCACCATCTTCCCTCCCGCCAGATGGTCAACAAG 463
Db 349 GCGGCGGTTTGAGGTGGGTGGCACCAGCACCTTCCCTCCCGCCAGATGATCAACAAG 408
QY 464 GTGTGCTCATGGGCGAGCAGATCATCCACGTGGCGGTCACTACCGTGTGGCTGTGGG 523
Db 409 GCATTCGCATGGGCAAGCCCATCATCCACGTGAGCTCAACTACCGGTGTGGCTGTGGG 468
QY 524 GGTTCCTGGCTGGTGCATGACATCAAGGCGGAGGCGAGGAAACCCCGCTTGAAGGACC 583
Db 469 GGTTCCTGGCTGGGCGAGATCAAGGCGGAGGCGAGTGCNAACGCCCGGTGAAGGACC 528
QY 584 AGCGTTTGGGATGACAGTGGGTGGCAGACAAATTTGCCGGGTTCGGCGCGACCCGAGCA 643
Db 529 AGCG - CTGGCATGACAGTGGGTGGGCGACAAATTTGGCGGTTCGGCGCGACCCGACCA 587
QY 644 AGGTGATCATCTTTGGCGAGTCTCGGCGCAGCATGTCCGTGTGTGGCCACCTCATCTGA 703
Db 588 AGGTGATCATCTTTGGCGAG - - - GCGGCGCAGCATGTCCGTGTGTGGCCACATCTCTCTGA 644
QY 704 ACGCGGCGCAACACAGGTACAGGCGCAAGCGGTGTTTCCGCGCGGCATCATGCAATCTG 763

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Db 645 AGACGGGACAAACGATCAAGGGCAAGCCGCTCTTCGCGCGGGCATCATGCGAG--G 701
Qy 764 GAGCCATGCTGCGCTCTGACCCGCGTGGACGCGACGTACGCGCAACGAGATCTACGACCTCT 823
Db 702 GGGCCATGCT---CGGGACGCTGGAGCGGTC-TACGGCAACGAGATCTTTGACCTCT 756
Qy 824 TTGCTCGAGTCTGCTGTGGCAGCGCCAGCGCAAGCTCGCTGCTTTGCGCAGTGGCT 883
Db 757 TGGCGTCTGA-CGCGGGCTGCGGCGAGCGCCAGCGCAAGCTTGGCTGCTTTGCGCGGTG- 814
Qy 884 CTAGCGACCTTGCTCGATGCCACCAACAACTCTCTGGGTCTTGGGTAATCTGCTGT 943
Db 815 --AGCGACAGTGTGAGGAGCGCCACCAACACCCCTGGGTCTTGGGTAATCTGCTGT 872
Qy 944 TCGCGTGTCTTATCTCCCGCGCGCGACGCGCAAGAACTACCGATGACATGATCAAGT 1003
Db 873 TCGGTTGTACT-----CCCCGCGCGCGCGGTGAACATACCGACGATGTGC---C 924
Qy 1004 TGGTGGCGACGCGCAAGTATGCAAGCGTTCCCGTGATCATTTGGCGACGACGAGG 1063
Db 925 TTGGTGGCGAGGCAAGTATGCA---CTCCTGTGATCATCGCGACGACGAGG 980
Qy 1064 GCACCATCTTTGGGCTCTCTTTTGAAGTGAACGACGAGTCTCAGGCGCGTGTACT 1123
Db 981 GCACCTTCTTTGG-----CACCTTGAACGTGACCAAGGATGCCAGGCGCGAG----- 1028
Qy 1124 TCAAGCAGTCTTTCATCCAGCGCGACGCGGAGATCGACACTTGTATGGCGGTGATCC 1183
Db 1029 TACTTCAGAGTGTGTCCAGCGCGAGCGCGAG--TCGACAGTGTGATGAGCGGTACT 1087
Qy 1184 CCCAGGACATCACCCAGGTTCTCGGTTGCAACGCGGTGTTCTCAACGCCCTCACCCGCG 1243
Db 1088 CC--GACATCACCCAGG-----CGTTTCGACACGGGT--TTCTCAAGGCCCTCACCCGCG 1139
Qy 1244 AGTTCAAGAGATCTCTGCGGTGCTCGGCGACTTGGCGACTTGTGATTCATCCAGCGCCGCGTACT 1303
Db 1140 AGTTCAAGAGATC---GCGGTGCTCGGCGACTTGTGTTAC-----GCCGTGCTACT 1189
Qy 1304 TCTCAACACACTTCCAGCGCGCACCAAGTACTCTGTTCTCTTAAGCAGTCTCTGGGT 1363
Db 1190 TCTCAACACACTTACACCGCGCGCACCAAGTACTCTATTCCTC-----AAGCAGTCTGGGT 1243
Qy 1364 TGCCAAATCATGGGCACTTCCATGCGCAACGACATTTGTGGCAGGACTACTTTGTTGGAA 1423
Db 1244 TGCGGTGCTCGGAAGTTTCACTCCACGACATTTGTTCCAGGACTACTTTGTTGGCA 1303
Qy 1424 GCGGAGCGGTCTATCAACAAACGCGTTTATCGCGTTGCGCAACCGACTTGGACCCCAACA 1483
Db 1304 GCGGTGCTCTATCTACAAACGCGTTTCAATGCGGTTTGCCACGAGCTTGGACCCCAACA 1363
Qy 1484 CCGCGGGTGTGTTGTTGAACTGGCCCAAGTACACGAGGCTCTCAGTCTGGCAACT 1543
Db 1364 CCGCGGGTGTGTTGTTGAACTGGCCGAGTACACGAGCAGC-----CAGGGCAACAACT 1417
Qy 1544 TGATGATGATCAACGCTTTGGGCTTTGTACACCGCAAGGACAACTTTCGCGACCGTGGCT 1603
Db 1418 TGATGATGATCAACGCTTTGGGCTTTGTACACCGCGCAAGGACAACT--TCGCGACCGCGGCT 1476
Qy 1604 ACGAGCGGTGTGATGACCAACCGCTTTCTTTT 1634
Db 1477 ACGAGCGGTGTGTTCTCCAACCGCGGTCTT 1507
```

RESULT 5

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US-11-061-894-1
; Sequence 1, Application US/11061894
; Publication No. US20050188439A1
; GENERAL INFORMATION:
; APPLICANT: McGutchen, Billy F.
; APPLICANT: Abad, Andre R.
; TITLE OF INVENTION: Methods for Enhancing Insect Resistance
; TITLE OF INVENTION: in Plants
```

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; FILE REFERENCE: 035718/286812
; CURRENT APPLICATION NUMBER: US/11/061,894
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,845
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: 60/546,533
; PRIOR FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic lipase from C. cylindracea; ctg codon
; OTHER INFORMATION: substituted for proper expression in plants
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1650)
US-11-061-894-1
```

```
Query Match 54.1%; Score 888; DB 24; Length 1650;
Best Local Similarity 71.7%; Pred. No. 5.6e-241;
Matches 1164; Conservative 0; Mismatches 460; Indels 0; Gaps 0;

Qy 17 GCCAGAGCGGCGCTCTCGGATCGGTACCCACGCGCAAGCTCGCCAAACGCGCGACACCATCA 76
Db 23 GCCTCATCGCAGCGTCTCGCGCGCCCGACCGCACCTCGCCAAACGCGCGACACCATCA 82
Qy 77 CCGGTCTCAACGCGCATCATCAACGAGGCGTTCTCTGGCATTTCCCTTTTCCGAGCGCGCG 136
Db 83 CCGGCTCAACGCGCATCATCAACGAGGCGTTCTCTGGCATTTCCCTTTTCCGAGCGCGCG 142
Qy 137 TGGGCAACTCTCGCTTCAAGGACCTTGCCTGCTACTCTGGCTCGTCTCAACGCGCGAAGT 196
Db 143 TGGGCAACTCTCGCTTCAAGGACCTCGGTCCCGTACAGCGCGAGCGCTCGACGCGCGAAGT 202
Qy 197 TCACCTTCTTACGCGCGCTTTCATGACAGAGAACCCCGAGGCGACGTTTGAAGAGAAC 256
Db 203 TCACAGTAGACGCGCGAGCTGCATGACAGAGAACCCCGAGGCGACCTTACGAGGAGAAC 262
Qy 257 TTGGCAAGACGCGCACTCGACTTGGTGTGATGCAAGTCCAAGTGTTCAGGCGGTCTTCCC 316
Db 263 TCCGAAAGCGCGCTCTCGACCTCGTCAATGACAGCAAGGTCTTCAGGCGCGTCAGCGCGA 322
Qy 317 AGAGTGAGGACTGCTCAACATCAACGTGCTCGCGCGCGCGGACCAAGCGCGGCGCA 376
Db 323 GCAGCGAGGACTGCTTCAACATCAACGTGCTGCGCGCGCGCGGCACTAAGCGCGCGCGCA 382
Qy 377 ACCTCCCGGTCTGCTCTGGATCTTTGGCGGTGGTGTGGATCGGACGCGCGCACCATCT 436
Db 383 ATCTGCTGTGATGCTGTGGATATTCGGGGGCGGCTTCGAAGTTCGAGGCGACCTCGAGT 442
Qy 437 TCCCTCCCGCGCAGATGCTCAACAGAGTGTGCTCATGGGCAAGCACATCATCAACGTGG 496
Db 443 TCCCGCGCGCCAAATGATAAAGTCTATAGCGATGGGGAAGCCAATATATACAGTCT 502
Qy 497 CGGTCAACTACGCTGTTCCTCTGCGGTTCCTTGGCTGGTGTGATGACATCAAGCGCGAG 556
Db 503 CAGTCAATTACAGGCTCAGTAGCTGGGTTTTCTCGCTGGAGATGAATCAAAAGCAGAGG 562
Qy 557 GCAGCGGGAACGCGGCTTGAAGGACCAAGCGTTTGGGCATCGAGTGGGTGGCGACAACA 616
Db 563 GCTCGCCCATCGCGGTTGAAGATCAAGGCTTGGTATGCAATGGGTGGCTGATATA 622
Qy 617 TTGCGCGGTTCCGCGCGCACCGGACGAGTGTACTATCTTTGGCGAGTCTTCGCGGCGACA 676
Db 623 TTGCGCGGTTTGGAGGCGATCCTACTAAAGTCAACATATTTGGGGAATTCGCGGCTCTA 682
Qy 677 TGTGCGGTTGTGCGACCTCATCTGGAACGAGCGGCAACAACATCAAGGCGCAAGCGGT 736
Db 683 TGTGAGTTATGTGTACATCTCTATGGAACGAGCGGAGATAATACGTACAAAGGCAACCGT 742
```

QY 737 TGTTCCGCGCGGCATATGTCAGTCTGGAGCCATGTCGCTGACCGGTGGACGCA 796
 Db 743 TATTTCCGCGCTGGATCATGCAAGTGGTGAATGTATGCCAGCATGCGTTCGATGAA 802
 QY 797 CCGTACGGCAACAGATCTACGACCTCTTTGCTCGAGTGTGGCTGTGGCAGCGCAGG 856
 Db 803 TCTATGGCAATGAGATCTTTGATGCTGCTCGCTCCAAATGCTGGGTGGGTTCGGCATCTG 862
 QY 857 ACAAGCTCGCGTCTGGCAGTGGTCTAGGAGCACCTTGTCTGATGCCACCAACACA 916
 Db 863 ATAAGTTGGCCCTTCGGGAGTGTCAAGTGATACATAGAGGATGCGACTAATAATA 922
 QY 917 CTCCTGGGTCTTTGGGCTACTCTCTGTTGGGTGTCTTATCTCCGGGCGCCGACGCA 976
 Db 923 CCCCAGGCTTTAGCTTATAGCTCCCTGGCTCTCTGTTTGTCTGACCGGAGGGG 982
 QY 977 AGAATCACCCGATGATGTAAGTGGTGGCGGACGCAAGTATGCAAGCGTTTCGG 1036
 Db 983 TGAACATTACGATGACATGTATGCACTTGTGAGAGAGGTAAATATGCCAATAATTCCG 1042
 QY 1037 TGATCATTTGGCCAGCAGACGAGGAGGCGACCATCTTTGGGCTCTTCTTTGAACGTGA 1096
 Db 1043 TGAATTTGGAGACAGACGAGGAGGACATCTTCGGGACTTTCTTCACTAAACGTCA 1102
 QY 1097 CCACGAATGCTCAGGCGCGTGTACTTCAAGCAGTCTTTTATCCAGCGCAGCGACGGG 1156
 Db 1103 CCACGAGCGCAAGCTAGGAGTACTTTTACAGAGTTTGTTCATGCAAGCGACGGG 1162
 QY 1157 AGATCGACACTTGTATGGCGGCTACCCCGAGGACATCACCCAGGGTTTCTCGGTTGACA 1216
 Db 1163 AGATTGACACATTAATGATGCTGCTACCCAGGTGACATTACCCAGGATCCCTTTGACA 1222
 QY 1217 CCGGTGTTCTCAAGCCCTCACCCCGCAGTTCAAGAGATCTCTGGGTGCTCGCGGACC 1276
 Db 1223 CCGGATCTCTGAACGCTCTCACACCGCAGTTTAAAGCGCATCTCGGCGATTTGGGGGACC 1282
 QY 1277 TTGCATTATCCACGCGCGCGCTACTTCTCAACCACTTCCAGGCGGCGACCAAGTACT 1336
 Db 1283 TTGGTTTCACTTAGCCCGCGTATTTCTTAAACCACTACACCGGAGGCGAGTACT 1342
 QY 1337 CGTTCTCTCTAAGCAGTCTCTGGGTGGCCAATCATGGGCACTTCCATGCGCAACGACA 1396
 Db 1343 CTCTCTCTCTCAAGCAGTCTCAGTGGCTTCCCGCTTGGTACATTCACAGCAACGACA 1402
 QY 1397 TTGTGGCAGACTACTTGTGGGAGCGGAGCGTCTATCAACACGCGTTTATCG 1456
 Db 1403 TCGTCTTCCAGGACTACCTGCTCGGATCCGGCTCTTATCTTACAAATATGCTTTTCAATG 1462
 QY 1457 CGTTCCGACCGACTTGGACCCCAACACGCGGGGTGTGGTGAACCTGGCCCAAGTACA 1516
 Db 1463 CTTCGCTACGATCTTGATCCAAATACGCTGGTCTTCTTGTAAAGTGGCCAGAGTACA 1522
 QY 1517 CCAGCAGTCTCAGTCTGGCAACAACTTGATGATGATCAAGCCCTTGGGCTTGTACACG 1576
 Db 1523 CATCTTCTCTCAGTCTGGTAATAATCTTATGATGAATTAATGCTCTTGGTCTTTACAGG 1582
 QY 1577 GCAAGCAGACTTCCGACCGCTGGCTAGGACGCTTGATGACCAACCGCTCTCTTCT 1636
 Db 1583 GTAAGGAATTTTCAAGACAGCTGGTTAGGATGCTTTTCTTCTTAATCAACCATCTTCT 1642
 QY 1637 TTGT 1640
 Db 1643 TCGT 1646

RESULT 6

US-11-061-233-1
 ; Sequence 1, Application US/11061233
 ; Publication No. US20050198706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCutchen, Billy F.
 ; APPLICANT: Abad, Andre R.
 ; APPLICANT: Wong, James F.

; APPLICANT: Yu, Guo Cao
 ; TITLE OF INVENTION: Lipases and Methods of Use
 ; FILE REFERENCE: 035718/286811
 ; CURRENT APPLICATION NUMBER: US/11/061,233
 ; CURRENT FILING DATE: 2005-02-18
 ; PRIOR APPLICATION NUMBER: 60/546,605
 ; PRIOR FILING DATE: 2004-02-20
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1650
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic lipase from C. cylindracea; ctd codon
 ; OTHER INFORMATION: substitution for proper expression in plants
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1650)
 US-11-061-233-1

Query Match 54.1%; Score 888; DB 24; Length 1650;
 Best Local Similarity 71.7%; Pred. No. 5.6e-241;
 Matches 1164; Conservative 0; Mismatches 460; Indels 0; Gaps 0;

QY 17 GCCCAGCGCGCTCTCGGATCGGTACCCACGCGCAAGCTGCCAACCGCGACACCATCA 76
 Db 23 GCCTCATCGCAGCGTCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 82
 QY 77 CCGGTCTCAACGCCCATCATCAACGAGGCGTTCCTCGGCATTCCTTTGCCGAGCGCGCG 136
 Db 83 CCGGCTCAACGCCCATCATCAACGAGGCGTTCCTCGGCATCCCGTTCCCGGAGCGCGCG 142
 QY 137 TGGGCAACCTCGGTTCAAGGACCTGTGCGTACTCTGTGCTCGCTCAACGGCGCAAGT 196
 Db 143 TCGGCAACCTCGGTTCAAGGACCTCGGTCGCTTACGCGGCGAGCTTCGACGGCGCAAGT 202
 QY 197 TCACCTCTTACGGCGCGTCTTGATGACAGAGAACCCCGAGGCGACGTTTGAAGAGAAC 256
 Db 203 TCACGAGCTACGGCCGAGCTGATGACAGAGAACCCCGAGGCGACCTTACGAGGAGAAC 262
 QY 257 TTGGCAAGCAGGCACTCGACTTTGGTGTGATGACAGTTCGAAGGTTCAGGCGGTGCTTCCC 316
 Db 263 TCCGGAAGCGCGCTCGACCTCGTCATGACAGAGCAAGTCTTCGAGGCGGTTCAGCCGA 322
 QY 317 AGATGAGGACTGCTTACCATCAACGTGTGCGGCGCGCGGACCAAGGGCGGCGCA 376
 Db 323 GCAGCGAGGACTGCTTACCATCAACGTGTGCGGCGCGCGGCACTAAGGCGCGCGCA 382
 QY 377 ACCTCCCGGTCTGCTCTGGATCTTTGGCGGTGGGTTCGATCGGACGCCCACTCT 436
 Db 383 ATCTGCTGTGATGCTGTGGATATTCGGGGGCGGTTTCAAGTTCGAGGCGACCTCGAGT 442
 QY 437 TCCCTCCCGCGCAGATGGTTCACCAAGAGTGTGCTCATGGGCAAGCACATCATCCAGTGG 496
 Db 443 TCCCGCGCGCAATGATATAAAGTCTATAGCGATGGGAAGCAATATATACAGTCT 502
 QY 497 CCGTCAACTACGTTGCTGCGGCGGTTCCTGGCTGGTGTGATGACATCAAGGCGGAGG 556
 Db 503 CAGTCAATTACAGGCTCAGTGTGGGTGCTGCTGGGAGATGAAATCAAAAGCAGAGG 562
 QY 557 GCAGCGGAACGCGCGCTTGAAGGACGAGCTTTGGGCGATGCGTGGGTGGCGAGACAACA 616
 Db 563 GCTCCGCATTCGGGGTTGAAGATCAAGGCTTGGTATGCAATGGGTGGCTGATATA 622
 QY 617 TTGCGGGTTCGGGCGGACCCGAGCAAGGTGACTATCTTTGGCGAGTCTTCGGGCGACA 676
 Db 623 TTGCAGCCTTTGGAGCGATCCTACTAAAGTCAACCATATTTGGGGAATCGGCGGTCTTA 682
 QY 677 TGTCCGTGTTGTGCCACCTCATCTGGAAACGAGGCGGCAACACGTTACAGGGCAAGCGT 736
 Db 683 TGTCAATTATGTGTGCATCTCTATGGAAACGAGGAGATAATACGTACAAAGCAACCGT 742

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QY 737 TGTTCGCGCGGCATCATGCGTCTGGAGCCATGTCGCTGTGACCCGGTGGACGCA 796
DB 743 TATTTTCGCGCTGGGATCATGCAAGTGGTGCATGTCACCGGATGCGGTGATGAA 802
QY 797 CGTAGGCAACAGATCTACGACCTTTTGTCTCGAGTGTGCTGTGCGAGCGGCGG 856
DB 803 TCTATGGCAATGAGATCTTTGATCTGCTCGCTGCAATGCTGGGTGCGGTTCGGCATCTG 862
QY 857 ACAAGTCTCGCTGTTCGCGAGTGGCTCTAGCGACACCTTGTCTGATGCGACCAACA 916
DB 863 ATAAGTTGCGCTTCCGCGAGTGTCAAGTGATACACTAGAGGATGCGACTAATATA 922
QY 917 CTCCTGGGTCTTGGGTAATCTCTGCTGGGTGCTTATCTCCGCGGCGCGACGCA 976
DB 923 CCCAGGCTCTTAGCTTATAGCTTCCGCTCTCTCGTATTTGCTGCTGACCGCGAGCGG 982
QY 977 AGAATCATCCGATGACATGTACAGTTGGTGGCGGCGCAAGTATGCAAGCGTTCCG 1036
DB 983 TGAACATACGATGACATGTATGCACTTGTGAGAGAGGTAAATATGCCAATATTTCCG 1042
QY 1037 TGATCATTTGGCGACAGAACGAGGCGACCATCTTTTGGGCTCTCTTTTGAACGTGA 1096
DB 1043 TGAATTTGGAGACAGACGAGGCGACATCTTCGGGACTTCTTCACTAAAGTCA 1102
QY 1097 CCACGAATGCTCAGGCGCGCTTACTTCAAGAGTCTTTTATCAACGCGCAGCGAGCGG 1156
DB 1103 CCACGAGCGCAAGCTAGGAGTACTTTAAGCAGAGTTTGTTCATGCAAGCGAGCGG 1162
QY 1157 AGATCGACACTTGTATGGCGGCTACCCCGCGAGTTCAGAGAACTCTCGGCTGCTCGCGACC 1216
DB 1163 AGATTTGACACATTAATGATCTGCTACCGAGTGAATTAACCGAGATCCCTTTTCGACA 1222
QY 1217 CGGCTGTCTTCAACCGCTCTACCCCGCGAGTTCAGAGAACTCTCGGCTGCTCGCGACC 1276
DB 1223 CGGCGACTCTGAACGCTCTCACACCGAGTTTAAGCGCATCTCGGAGTATTTGGGGAGC 1282
QY 1277 TTGCATTTCAACCGCGCGCTACTTCTCTCAACACTTTCAGGCGCGCACCAAGTACT 1336
DB 1283 TTGGTTTCACTTAGCGCGCGCTTATTTCTTAAACCACTACACCGGAGCGACGAAGTACT 1342
QY 1337 GGTTCCTCTTAAGCAGCTCTGCGGTGCGCAATCATGGGACCTTCCATGCGCACGACA 1396
DB 1343 CTTCCTGTCAAAGCAGCTCAGTGGCTTGCCTGCTTGGTACATTCACACGACCAACGACA 1402
QY 1397 TTGTGTGGCAGACTACTTGTGGGAAGCGGCGAGCGTCACTTACAAACAGCGGTTTATCG 1456
DB 1403 TCGTCTTCCAGACTACTCTGCTCGGATCGGCTCTTATCTTACAAATATGCTTTCATG 1462
QY 1457 CGTTCCGCAACGACTTTGGACCCCAACACGCGGGGTGTTGGTGAACCTGGCCCAAGTACA 1516
DB 1463 CTTTCGCTACGATCTTGATCCAAATACGGCTGGTCTTCTTGTAAAGTGGCCAGAGTACA 1522
QY 1517 CCAGCAGCTCAGTCTGCAACACTTGATGATGATCAACGCTTGGGCTGTGACACCG 1576
DB 1523 CATCTTCTCAGTCTGGAATAATCTTATGATGAATTAAGTCTCTTGGTCTTTTACACGG 1582
QY 1577 GCAAGGCAAACTTCGCGACCGCTGCTAGCGCGTGTGATGACCAACCGCTCTCTTTCT 1636
DB 1583 GTAAGGATAATTTACAGACAGCTGTGTAGATGCTCTTTCTTCTAATCCCAATCTTCT 1642
QY 1637 TTGT 1640
DB 1643 TCGT 1646
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RESULT 7

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US-09-943-857-1
; Sequence 1, Application US/09943857
; Publication No. US20030124701A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Jei-Fu
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Jye
```

```
; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943,857
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1469
; TYPE: DNA
; ORGANISM: Candida rugosa
US-09-943-857-1
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Query Match 47.4%; Score 778.4; DB 10; Length 1469;
Best Local Similarity 75.7%; Pred. No. 6e-210;
Matches 1200; Conservative 0; Mismatches 261; Indels 125; Gaps 14;
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QY 51 CAAGCTCCGCAACGGCGACACCATCACCGGTCTCAACGCCATCATCAAGAGCGGTTCCT 110
DB 8 CCACCTCGCCAAACGGCGACACCATCACCGGTCTCAACGCCATTTGTCAACGAAAGTTTCT 67
QY 111 CGGCATTCCCTTTTGCAGCGCGCGGTGGGCAACCTCGCTTCAAGGACCCCTGTGCCGTA 170
DB 68 CGGCATACCGTTTGCAGAGCGCGCGGTGGGCA--CTCCGCTTCAA-----110
QY 171 CTCTGGCTCGCTCAACGGCGCAGAAAGTTTCACTTTTACGGCGCGCTTGTGATGACAGAGAA 230
DB 111 -----GCTCAACGGCGCAGAGTTTAC-----CTACGGCGCGTGCATGACAGTAA 155
QY 231 CCCGAGGCGCAGTTTGAAGAGAACCTTGGGCAAGACGGCACTCGACTGTGGTGTGATGAGTC 290
DB 156 CCTATGGGCTCGTTTCA-----187
QY 291 CAAGGTGTTCCAGCGCGGTGCTTCCCGAGGTGAGGACTCGCTCACCATCAACGTGGTGG 350
DB 188 CAAGATCTTCAAGTGTGCTTCCCAAGCAGAGGACTGTCTCAC-----232
QY 351 CGCGCGGCGCACCAAGCGCGCGCGCAACCTCCCGGTCACTGTCTGGATCTTTGGCGGTGG 410
DB 233 -----CACCAGGGCGCAGTGTGCTTCCCGGTGATGCTTGGATCTTTGGCGGTGG 283
QY 411 GTTTGAGATCGGCGAGCCCCACCATCTTCCCTCCCGCCAGATGTFCAACAAGATGTGCT 470
DB 284 GTTTGAGCTTGGCGCTCCAGCTCTTTTCCAGGAGACCAAGATGTTGGTGGCAAGAGCGTGT 343
QY 471 CATGGCAAGCACATCATCCACGTGGCGTCAACTACCGTGTGCTCGTGGGGTCTT 530
DB 344 CATGGTAAACCGGTGATCCACGTGAGCATGAACCTACCGGTGGCGTCAATGGGGTCTT 403
QY 531 GGCTGGTGAATGACATCAAGGCGGAGGCGAGGAAACCGCGGCTTTGAAGGACACAGCTTT 590
DB 404 GGCGGCGCGCGACATCCAGAACGAGGAGCGAGCGCGGCTTGCATGACACGCGCTT 463
QY 591 GGGCATGAGTGGGTGGCAGACAACATTTGCGGGTTGCGGGGCGAGCCCGAGCAAGGTGAC 650
DB 464 GGCCATGAGTGGGTGGCGGCAACAATTTGCTGGGTGGCGGCGACCCCGAGCAAGGTGAC 523
QY 651 TATCTTTGGCGAGTCTGGCGCAGCATGCTCGTGTGTGGCCACCTCATCTGGAACGACGG 710
DB 524 CATATACGGCGAG---GCGGGCAGCATGTCAGCTTTGTGACCTTTGTGGAACGACGG 580
QY 711 CGACAACAAGTACAAGGGCAAGCGGTTTTCGCGCGGGGCATCATGCACTGTGGAGCCAT 770
DB 581 CGACAACAAGTACAAGCGGAGCGGTTTTCGCGCGCGCCATCATGCA-----GGCTG 634
QY 771 GGTGCGCTGACCCCGGTGGAGCGGACGTACGGCAACGAGATCTACGACCTCTTTGTCTC 830
DB 635 CATGTGCGGACCCCGGTGGAGCGGACGTACGGCAACGAGATCTACACCAAGGTGGTGGC 694
QY 831 GAGTGTGGCTGTGCGAGCGCCAGGCAAGCTCGCGTGTGCGAGTGGTGTAGGCA 890
DB 695 GTCTGCCGGGTGTGGCAGTGTGCGAGCAAGCTCGCGTGTGCGGCGCTTTTCTCAGA 754
QY 891 CACCTTGTGATGCCACCAACACACTCTCTGGGTCTTTGGCGTACTCTCTGTTGCGGTT 950
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[illegible]

RESULT 8
US-10-369-493-27923
; Sequence 27923, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 27923
; LENGTH: 1687
; TYPE: DNA

i ORGANISM: *Neurospora crassa*
 US-10-369-493-27923

	Query Match	21.6%	Score 354.2;	DB 17;	Length 1687;
	Best Local Similarity	55.7%	Pred. No. 9e-90;		
	Matches 811; Conservative	0;	Mismatches 573;	Indels 73;	Gaps 4;
Qy	66	CGACACCATCACCGGTCTCAACGCCATCATCAACGAGGCGTTCCTCGGCATATCCCTTTTGC	125		
Db	27	CGGTACGATTGTGGTGTAAAGGCATCTCTCATGAGGCCCTTCAACGGATATCCCTTACGC	86		
Qy	126	CGAGCCGCCGGTGGGCAACCTCCGCTTCAAGGACCCCTGTGCCGTACTCTGGCTCGCTCAA	185		
Db	87	CTTTCTCCGACCGGCAACCTCCGCTCAAGCCCTCCGCTGAGACTTAAAGTCGTCTCTGGG	146		
Qy	186	CGGCCAGAGTTCACTTCTTAACGCCCGGTCTTGGATGACGACAGAAACCCGAGGGCAGTT	245		
Db	147	TGTTCTTTGATGCGTCTGSCATCGGCCCTGTGTCGCCCACTTCTCTTGTCTGACACCTCGTC	206		
Qy	246	TGAAGAGAACTTTGGCAAGACGCGACTCGACTTGGTGATGACGTCCAAAGGTGTTCCAGGC	305		
Db	207	GACGAGTTTCTGGCTCA----GGTTATCGATAAGATGTTAAACGGCAGCTTTTCAAGAC	263		
Qy	306	GGTGCTTTCCCGAGATGAGGACTGCCTCACCATCAAGCGTGTGGCGCGCGGGCACCAA	365		
Db	264	TATACTCAACGTCAAGGAGGACTGCTTGACCATCTCGGTCACTCGTCCCAAGGGCACCA	323		
Qy	366	GGGGGGCGCAACCTCCCGGTCACTCTGGATCTTTGGCGGTGGGTTTG-----	415		
Db	324	GGCTGGTGATAAGCTCCCGCTCTTTTCTGGATCTTTGGTGTTGGTTTCCGAAGTGAGAA	383		
Qy	416	-----AGATCGGCAGCCCCA	430		
Db	384	TCCAGCTTATACGCGATGTAATGAACAAGTCTAAACTTCACAGCTCGGATCGCGGT	443		
Qy	431	CCATCTTTCCCTCCCGCCAGATGCTCACCAAGAGTGTCTCATGGGCAAGCACATCATCC	490		
Db	444	CCATGTACGATGCGCTCCCTAGTCACCAACGCTATCAACATGGGTAAAGCCGTGCTCT	503		
Qy	491	ACGTGGCGGTCAACTACCGTTGTCCTCTGCGGGGTCTTGGCTGGTGATGACATCAAGG	550		
Db	504	ACGTGCGGTCAACTACCGTGTCTCGGTGGCTTTGTTTCATGCCCGGAAAGGAGATCCTTA	563		
Qy	551	CCGAGGSCAGCGGAACCGCGGCTTGAAGACACAGCGTTTGGGCATGCACTGGTGGCAG	610		
Db	564	AGGACGCTCTTCCAACTTGGGTCACTTGACACAGCGCATGGCGCTCCAGTGGTGGCG	623		
Qy	611	ACAACATTGCGGGTTTCGGCGGACCCGAGCAAGGTGACTATCTTTGGCGAGTCTGCGG	670		
Db	624	ACAACATTGCGCTTCGGCGGTGACCCAGCAAGGTCACTATCTGGGCGAGTCCGCGC	683		
Qy	671	GCAGATGTCGTGTGTGTCACCTCATCTGGAACGACGCGCGACACACGTACAGGGCA	730		
Db	684	GTGCCATGTCGGTTTTTCAACACAGATGTCTCTCTATGACGCTGACACACGTACACGGCA	743		
Qy	731	AGCGTTGTTCCGCGGGGACATACGAGTCTCGAGCCATGNGCGCTCTGACCCCGTGG	790		
Db	744	AGCCCCCTTTCCGTTGGCGCCATCATGAATCTCTGGTTCATCTCCCGCGGCCCGTCG	803		
Qy	791	ACGSCAGTACGGCAACGAGATCTAGACCTCTTTGTCTCGAGTGTGGCTGTGGCAGCG	850		
Db	804	ACTGCCCAAGSGCCAGAAAGTCTACGACACCGTCTGTAAGAACGCGCGTCTCTGGTG	863		
Qy	851	CCAGCGACAGCTCGGTGTCTGGCAGTGCCTGTAGCGACACCTTGTCTCGATGCCACCA	910		
Db	864	CTGTGACACCTTGTCTGCTCGCGGCTCTTCCCTACGAGACTTTTCTCAAGGCCGCTA	923		
Qy	911	ACAACTCTCTGGTCTTTCGCGTACTCTCTGTTTGGGTTGTCTTATCTCCCGCGGCCG	970		
Db	924	ACTCCGTGCTGGATTCTGTGTGTAACATCCGTTGTCTTTCTTACCTCCCGGACCGG	983		
Qy	971	ACGSCAAGAACATCACCGATGACATGATACAAAGTTGGTGGCGGACGGCAAGTATGCAAGCG	1030		

Db 984 ATGGCAAGGCTTTGACTCAGAGCGCGGATGAAGCTCATGCTCGCTAAGAGTACGCGCGCG 1043
QY 1031 TTCCCGTGATCATTTGGCGACAGAACGACGAGGCGCACATCTTTGGGCTCTCTCTTTGA 1090
Db 1044 TCCCATGATCATCGGCGGATCAAGAGGATGAGGCGACTCTCTTCTCCCTCTTCCAGGCA 1103
QY 1091 ACCTGACCAAGATGCTCAGGCGGCTGCTTACTTCAAGCAG----TCTTTCAATCCAGGCA 1147
Db 1104 ACATCACCAACCAAGCAAGCTGGTCAGCTACCTCAACGATATCTTCTTCAACGAGGCA 1163
QY 1148 GCGACGCGGAGATCGACACCTTGTATGCGGCGGTACCCAGGACATCACCCAGGTTCTC 1207
Db 1164 CCGAGTGCAGATTAAGTCTCTGCTCGTACCTTACAGTACCTTATCTCGCGGCTCGC 1223
QY 1208 CGTTGACACGGGTGTTCTCAACGCGCTCACCCCGGAGTTCAAGAGAACTCTTCGCGGTG 1267
Db 1224 CTTTGGCACCGGCTCTTCAACGAGATTTACCCCGGCTTCAAGCGCTTGGCGGCAATTC 1283
QY 1268 TCGGCACTTGCATTCATTCACGCGCGGCTTACTTCTCTCAAC-----CACT 1315
Db 1284 TTGGCGATCTCATCTTTCACCCCTCAGCGCGCGCATCTTCTCGACGCGCGCACCACTCTCA 1343
QY 1316 TCCAGGCGGCGACCAAGTACTGTTCTCTCTTAAGCAGCTCTTGGGTTGCCAATCATGG 1375
Db 1344 ACCCTCGGTGCGCGCTGGTGTATCTTGGCTTACAACTTTGGCACACCCATCCTTG 1403
QY 1376 GCACCTTCCATGCCAACGACATTTGTGTGGCAGGACTACTTGTGGGAAGCGGAGGTCA 1435
Db 1404 GAACCTTTACGCGCTCGGATATCTCGAGGTGTTCTACGGCATCTTGGCCCAACTAGGCA 1463
QY 1436 TCTAACAACAGCGTTT 1452
Db 1464 GCAAAAGCATCCAGTCT 1480

RESULT 9

US-09-801-852A-1
; Sequence 1, Application US/09801852A
; Patent No. US20020048781A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Chiang, Shu-Jen
; APPLICANT: Jonathan, Basch
; TITLE OF INVENTION: DIRECT PRODUCTION OF DESACETYLCEPHALOSPORIN C
; FILE REFERENCE: ON0163
; CURRENT APPLICATION NUMBER: US/09/801,852A
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/188,033
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Rhodospiridium toruloides
US-09-801-852A-1

Query Match 7.3%; Score 119.6; DB 9; Length 1716;
Best Local Similarity 53.8%; Pred. No. 2.6e-23;
Matches 301; Conservative 0; Mismatches 244; Indels 15; Gaps 2;
QY 322 GAGGACTGCTCACCATCAACGTGTGCGCGCGCGGCAACGAGCGGCGGCCCAACCTC 381
Db 361 GAGGATTGCTCTTCTCTCAATGCTGTGCGCGCGCGGCTCGTGGAGGCGCAATCTT 420
QY 382 CCGGTATGCTCTGATCTTTGGCGGTGGGTTTGAATCGGAGCCGCCACCACTTTCCT 441
Db 421 CCGGCTCTGCTACATTCACGAGGTGGCTACGCGCTTTCGGGATGCGAGCACCGCGAGC 480
QY 442 CCGCGCCAGATGGTACCAAGAGTGTGCTCATGGGCAACACATCATCCAGTGGCGCTC 501
Db 481 GACTTTGGCGCTTACCAA-----GCACGCGGAACCAAGATGGTGTGTAATCTC 534

QY 502 AACTACCGTGTGCTCTGCGGGGTTCTTGGCTGTGTGATGATCAATCAAGGCCGAGGCGCAG 561
Db 535 CAGTACCGTCTCGGAGCTTTGGTTTCTCGCTGGCCAAAGCCATGAAGACTACGGTGTGA 594
QY 562 GGGAAAGCCCGGCTTGAAGGACCAAGCGTTTGGGATGACGTGGGTGGCAGACAACATTTGCC 621
Db 595 ACBAAGCCCGGCTTGTGACCAAGAAATTCGCCCTTCAATGGGTTTCAACAGCACGCTCTCG 654
QY 622 GGGTTGCGGCGGACCCGAGCAAGGTACTATCTTTGGGAGTCTGCGGCGGAGCATGTCTC 681
Db 655 AAGTTGCGGCGCAACCCCGATCAGTTAGATTTGGGCGAGTCTTCAGGCGGAGGTTCC 714
QY 682 GTGTTGTGCACCTCATCTGGAACGACGCGGCAACAACGTAACAAGGC-----AAG 732
Db 715 GTTATGAACACGATCATTCGGAACGCGGCGCAACACCGTCAAGGCTCTCGGTCTCAAGAAG 774
QY 733 CGGTTGTTCCGCGCGGCGCATCATGAGTCTTGAGGCCATGTTGCCGCTCACCGGTGGAC 792
Db 775 CCGCTCTTCCAGCTGCCATCGGCTCTCGCTTCTCCCTTACCAAGCCAAGTACAAC 834
QY 793 GGCAGTACGCGCAACGAGATCTACGACCTCTTTGTCTCGAGTGTGGCTGTGGCAGCGCC 852
Db 835 TCCCGCTTTCGCGAGTGTCTTACTCCCAACTCGTCTCGGCGCAAACTGCACCAAGGCC 894
QY 853 AGCGACAAGCTCGCGTGTCT 872
Db 895 GCCTCGTCTCTCGCTTGCT 914

RESULT 10

US-10-369-493-41665
; Sequence 41665, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 41665
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: SPHINGOMONAS
US-10-369-493-41665

Query Match 6.3%; Score 103.8; DB 17; Length 1272;
Best Local Similarity 53.4%; Pred. No. 7.1e-19;
Matches 241; Conservative 0; Mismatches 207; Indels 3; Gaps 1;

QY 322 GAGGACTGCTCACCATCAACGTGTGCGCGCGCGGCAACGAGCGGCGGCCCAACCTC 381
Db 223 GAGGACTGCTGTATCTCAACGTGTGGAGGCGCGCGCGCGCGCGCGCGCGCGCTG 282
QY 382 CCGGTATGCTCTGATCTTTGGCGGTGGGTTTGAATCGGCG--CCCAACCATCTTC 438
Db 283 CCGGTATGCTGTGATGATGAGTCTAGCGCGCGGATTCGTGAACCGCGGTGCTCTCCCCCACC 342
QY 439 CTTCCGCGCCAGATGGTCAACAAGTGTGCTCATGGGCAAGCAATCATCCAGTGGCC 498
Db 343 TATGCGGCGCAACCTGGCGAAGCAGGCGGTGCTGTTGTCAGCTTCAACTACCGGCTC 402
QY 499 GTCAACTACCGTGTGCTCGTGGGGTCTTGGCTGTGTGATGATCAAGGCCAGGCGC 558
Db 403 GGCGCTTTCGCGAGCTTCGCCCTCTCCGCAACTCAGCGCGGAAGACGCGGATGGCGGGCTG 462

QY 890 ACACCTTGTCTGATGCCAACCAACACTTCCTGGGTTCTTGGGTACTCTCTGTTGCGT 949
Db 923 CAGCGCAGGTCTCTGTGTGAACACCAATGGCACTGCTGCTCAAGAAAGCGTCTTCCGCT 982
QY 950 TGTCTTATCTCCCGCGCCGCGGCAAGAACATACCGATGACATGTACAAGTTGGTGC 1009
Db 983 TCTCTTCTGCTGTGTGTAGATGGAGACTTCTCTAGTGACACCCAGAGGCCCTCATCA 1042
QY 1010 GCGACGGCAAGTATGCAAGCGTTTCCCGTGATCATTTGGCGACACGAGGGCACCA 1069
Db 1043 ACGCGGAGACTTCCACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1102
QY 1070 TCTTTGGGCTCT 1081
Db 1103 ATTTTCTGGTTT 1114

RESULT 13

US-10-792-491-5
; Sequence 5, Application US/10792491
; Publication No. US20040148657A1
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Mor, Tsafir S.
; APPLICANT: Arntzen, Charles J.
; APPLICANT: Mason, Hugh S.
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
; TITLE OF INVENTION: TRANSGENIC PLANTS
; FILE REFERENCE: BTI-45
; CURRENT APPLICATION NUMBER: US/10/792,491
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/190,440
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 3.1
; SEQ ID NO 5
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: human acetylcholinesterase gene optimized for
; OTHER INFORMATION: expression in plants
US-10-792-491-5

Query Match 4.5%; Score 74.4; DB 22; Length 1725;
Best Local Similarity 47.1%; Pred. No. 1.6e-10;
Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;
QY 290 CCAAGGTGTTCCAGGCGGTGCTTCCCGCAGAGTGAGGACTGCTCACCATCAACGTGGTGC 349
Db 341 CCGAGATGTGGAACCCCAACCGTGAGCTGAGCGAGGACTGCTGTACCTCAAC---GTGT 397
QY 350 GCGCGCGGGGCAACGAAGCGGGCGGCAACCTCCCGGTATGCTCTGGATCTTTGGCGGTG 409
Db 398 GGACACCATACCCCGGCGCTACATCCCGCCCTGCTCTCTGATCTATGGGGGTG 457
QY 410 GGTGTTGAGTCCGAGCGCCACCATCTCCCTCCCGCCAGATGTCACCAAGATGTGC 469
Db 458 GTTCTTACAGTGGGCGCTCTCTTGGAGCTGTACGATGGCGCGCTTC-----TTGG 508
QY 470 TCATGGGCAAGCACATCATCCACGTGGCGGTCAACTACCGTGTGTGCTCTGTTGGGGGTCT 529
Db 509 TACAGGCCGAGAGGACTGTGCTGTGTCTCATGAACTACCGGTGGGAGCTTTGGCTTCC 568
QY 530 TGGCTGTGATGACATCAAGCGCGGAGGCGAGGAAACCGCGCTTTGAAGGACCAAGCTT 589
Db 569 TGGCCCTCGCGGGGAGC---CGAGAGGCGCCGGGCAATGTGGCTCTCTGGATCAGAGGC 625
QY 590 TGGGCTACAGTGGGTGGCAGACATGTCGGGTTCGGCGGCGACCGGACCAAGGTGA 649
Db 626 TGGCCCTGAGTGGGTGACGAGGAACGTGGGCGCTTTCGGGGGTGACCCGACATCAGTGA 685

QY 650 CTATCTTTGGCGAGTCTGCGGCGACATGTTCGTTGTGTGCGACCTCATCTGGAACGAG 709
Db 686 CGCTGTTTGGGAGAGCGCGGAGCGGCTCGTGGGATGACCTGTCTGCCGCCCA 745
QY 710 GCGCAACACAGTACAAAGGGCAAGCGGTTGTTCCGCGCGGGCATCATGCAAGTCTGAGGCCA 769
Db 746 GCGCGGGGCTGTTCACACAGGGCGGTGCTGCAAGAGCGGTGCCCCCAATGGAACCTTGGGCCA 805
QY 770 TGGTCCCGTCTGACCCCGTGGACGCGCATGACGGCAACGAGATCTACGACCTCTTTGTCT 829
Db 806 CGGTGGGATGAGGAGAGGCCCGTCCAGG---GCCACGAGCTGGCCACCTCTGTGGGT 862
QY 830 CGAGTGTGGTGTGGCAGCGCCAGCAAGCTCCGCTGTGTTGGCAGTGGCTCTAGCG 889
Db 863 GTCTCCAGGCGGCACTGTGGGAATGACACAGAGCTGGTAGCTGCTTCCGACACGAC 922
QY 890 ACACCTTGTCTGATGCCAACCAACACTCTCTGGGTTCTTGGCGTACTCTCTGTTGCGT 949
Db 923 CAGCGCAGGTCTCTGTGTAACCAACGAAATGGCAGTCTGCTCAAGAAAGCGTCTTCCGCT 982
QY 950 TGTCTTATCTCCCGCGGCGCGGCAAGAACATCACCGATGACATGTACAAGTTGGTGC 1009
Db 983 TCTCTTCTGCTGTGTGTAGATGGAGACTTCTCTAGTACACCCAGAGGCCCTCATCA 1042
QY 1010 GCGACGGCAAGTATGCAAGCGTTTCCCGTGATCATTTGGCGACACGAGGGCACCA 1069
Db 1043 ACGCGGAGACTTCCACGGCTGACGAGTGTGCTGGTGGTGTGTTGAAGATGAGGGCTCT 1102
QY 1070 TCTTTGGGCTCT 1081
Db 1103 ATTTTCTGGTTT 1114

RESULT 14

US-10-887-553A-108
; Sequence 108, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; TITLE OF INVENTION: with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 2909
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-108

Query Match 4.5%; Score 74.4; DB 21; Length 2909;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;
Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;
QY 290 CCAAGGTGTTCCAGGCGGTGCTTCCCGCAGAGTGAGGACTGCTCACCATCAACGTGGTGC 349
Db 435 CCGAGATGTGGAACCCCAACCGTGAGCTGAGCGAGGACTGCTGTACCTCAAC---GTGT 491
QY 350 GCGCGCGGGGCAACGAAGCGGGCGGCAACCTCCCGGTATGCTCTGGATCTTTGGCGGTG 409
Db 492 GGACACCATATACCCCGGCGCTACATCCCGCCACCTGCTCTCTGATCTATGGGGGTG 551
QY 410 GGTGTTGAGTCCGAGCGCCACCATCTTCCCTCCCGCCAGATGCTCACCAGAGTGTGC 469
Db 552 GTTCTACAGTGGGGCTCTCTCTTGGAGCTGTAGATGGCGCGCTTC-----TTGG 602
QY 470 TCATGGGCAAGCACATCATCCACGTGGCGGTCAACTACCGTGTGCTCTGCGGGGTCT 529

Db 603 TACAGCCGAGAGGACTGTGCTGCTCCATGAATACCGGGTGGAGCCTTTGGCTTCC 662
 QY 530 TGGCTGGTATGATCAAGCCGAGCGGGAACCGCGCTTGAAGGACGACGTT 589
 Db 663 TGGCCCTGCGGGGAGC---CGAGAGGCCCGGGCAATGTGGTCTCTCTGGATCAGAGC 719
 QY 590 TGGGCATGAGTGGGTGGCAGCAACATTTGCCGGTTTCCGGCGGCGACCCGAGCAAGGTGA 649
 Db 720 TGGCCCTGAGTGGGTGGCAGGAACTGTGGAGCCTTCCGGGGTGAACCCGACATCAGTGA 779
 QY 650 CTATCTTTGGGAGTCTGCGGGCAGCATGTCCGTGTTGTGCCACTCATCTGGAACGAGC 709
 Db 780 CGCTGTTTGGGAGAGCGCGGAGCGCCTCGTGGGCATGACCTGTCTCTCCCGCCCA 839
 QY 710 GCGACAACAGCTACAGGGAAGCGTTGTTCCGGCGGGGACATCATGAGTCTGGAGCCA 769
 Db 840 GCGGGGCGCTGTTCACAGGGCGGTGCTGCAGAGCGGTGCCCCCAATGGACCCCTGGGCCA 899
 QY 770 TGGTGGCGTCTGACCCGGTGGAGCGCATGTCAGGCAACGAGATCTACGACCTCTTTGTCT 829
 Db 900 CGGTGGGCATGGAGAGGCCCTCGCAGG---GCCACGAGCTGGCCCACTTGTGGCT 956
 QY 830 CGAGTCTGGTGTGGCAGCGCCAGCAAGCTCGCGTGTGGCGAGTGGCTCTAGCG 889
 Db 957 GTCTCCAGCGGCACTGTGTGGAAATGACACAGAGCTGTAGCTGCTTGGGACACGAC 1016
 QY 890 ACACCTTGTGATGCCCAACAAACACTCTCTGGGTTCTGGGCTACTCTCTGGTGGGT 949
 Db 1017 CAGCGCAGGTCTCTGTGGAAACCAAGATGGCAGCTGTCTCAAGAAAGCTCTTCCGCT 1076
 QY 950 TGTCTTATCTCCCGCGCCGCGGCAAGAAATACACCGATGACATGTACAAAGTTGGTGC 1009
 Db 1077 TCTCTCTGCTGTGTGTAGATGAGACTTCTCAGTGACACCCAGAGGCCCTCATCA 1136
 QY 1010 GCGACGGCAAGTATCAAGCTTCCGCTGATCATTTGGCGACCAAGACGAGGGGACCA 1069
 Db 1137 ACGCGGAGACTTCCACGCGCTGCAGGTCTGTGGTGTGTGGTGAAGGATGAGGCTGT 1196
 QY 1070 TCTTTGGGCTCT 1081
 Db 1197 ATTTCTGGTTT 1208

RESULT 15
 US-09-810-861B-3
 ; Sequence 3, Application US/09810861B
 ; Patent No. US20020162140A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mor, Tsafir S.
 ; APPLICANT: Soreq, Hermona
 ; APPLICANT: Arntzen, Charles J.
 ; APPLICANT: Mason, Hugh S.
 ; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
 ; TRANSGENIC PLANTS
 ; FILE REFERENCE: BTI-45
 ; CURRENT APPLICATION NUMBER: US/09/810,861B
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/190,440
 ; PRIOR FILING DATE: 2000-03-17
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 3
 ; LENGTH: 5767
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: plasmid vector
 ; OTHER INFORMATION: pTW034.
 US-09-810-861B-3

Query Match 4.5%; Score 74.4; DB 9; Length 5767;
 Best Local Similarity 47.1%; Pred. No. 2.2e-10;
 Matches 373; Conservative 0; Mismatches 401; Indels 18; Gaps 4;

QY 290 CCAAGTGTTCAGGCGGTGCTTCCCGAGGTAGGACTGCCTCACCATCAAGTGGTGC 349
 Db 1178 CCGAGATGTGAACCCCAACCGTGAAGTGAAGGAGTGCCTGTACCTCAAC---GTGT 1234
 QY 350 GSCCGCCGGGACCAAGGCGGCGCAACCTCCCGGTCAATGCTCTGGATCTTTGGCGGTG 409
 Db 1235 GGAACACATACCCCGGCTCATATCCCAACCCCTGCTCTGTCTGGATCATATGGGGTG 1294
 QY 410 GGTTTGAGATCGGCAAGCCCAACATCTTCCCTCCCGCCAGATGTCACCAAGAGTGTGC 469
 Db 1295 GCTTCTACAGTGGGGCTCTCTTGGACGTGTACGATGGCGGCTTC-----TTGG 1345
 QY 470 TCATGGGCAAGCATCATCATCCAGTGGCGGTCAATACGTTGCTGTGGGGGTCT 529
 Db 1346 TACAGGCGAGAGGACTGTGTGTGTCTCATGAATACCGGTGGGAGCTTTGGCTTCC 1405
 QY 530 TGGCTGGTGTACATCAAGGCGGAGGAGCGCGGCAACCGCGCTTGAAGGACACGCTT 589
 Db 1406 TGGCCCTGCGGGGAGC---CGAGAGGCCCGGGCAATGTGGGTCTCTGATCAGAGC 1462
 QY 590 TGGGCATCAGTGGGTGGCAGACAAATTGCCGGGTTCGGCGGCGACCCGAGCAAGTGA 649
 Db 1463 TGGCCCTGAGTGGGTGCAGGAGAACGTGGCAGCCTTCGGGGGTGACCCGACATCAGTGA 1522
 QY 650 CTATCTTTGGCGAGTCTCGGGCAGCATGTCCGTGTGTGGCCACTCATCTGGAACGAGC 709
 Db 1523 CGCTGTTTGGGAGAGCGCGGAGCGCTCGTGGGCAATGCACCTGTGTCTCCCGCCCA 1582
 QY 710 GCGACAACATGTAAGGCGCAAGCGTTGTTCCCGCGCGGCATCATGCACTCTGGAGCA 769
 Db 1583 GCGGGGCTGTTCACAGAGGCCGTGTGACAGGGGTGCCCCNATGGACCTGGGGCA 1642
 QY 770 TGGTGGCTGTGACCCCGTGGACGCGTACGCAACGAGATCTACGACCTTTGTGT 829
 Db 1643 CGGTGGGCATGGAGAGGCCCGTGCAGG---GCCACGAGCTGGCCCACTTGTGGCT 1699
 QY 830 CGAGTGTGGCTGTGGCAGCGCCAGCAAGCTCGCGTGTGGCGAGTGGTCTAGCG 889
 Db 1700 GTCTCCAGGGCGCATGTGTGGGAATGACACAGAGCTGTAGCTGCTCGGACACGAC 1759
 QY 890 ACACCTTGTCTGATGCCACCAACACTCTCTGGGTCTTGGCGTACTCTCTGCTTGGCT 949
 Db 1760 CAGCGCAGTCTGTGTGAACCAACGAAATGGCAGCTGTGCTCAAGAAAGCTCTTCCGT 1819
 QY 950 TGTCTTATCTCCCGCGCCCGACGCAAGAACATCACCGATGACATGTACAAAGTGGTGC 1009
 Db 1820 TCTCTTCTGCTGTGTGTAGATGAGACTTCTCAGTGACACCCCGAGGCGCTCATCA 1879
 QY 1010 GCGAGCGCAATGCAAGCGTTCCCGTGTATCATTTGGCGACCAAGAACGAGGGGACCA 1069
 Db 1880 ACGCGGAGACTTCCACGCGCTGCAGGTGTGTGGGTGTGGTGAAGGATGAGGGCTCGT 1939
 QY 1070 TCTTTGGGCTCT 1081
 Db 1940 ATTTCTGGTTT 1951

Search completed: September 22, 2005, 10:32:41
 Job time : 1750 secs

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OM protein - protein search, using sw model

Run on: September 17, 2005, 07:32:23 ; Search time 43 Seconds
(without alignments)
949.606 Million cell updates/sec

Title: US-09-943-857A-4
Perfect score: 2864
Sequence: 1 SMNSKGPAGRLGVSFTAKLA.....DNFRTAGYDALMTNPSSFFV 547

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1107	38.7	563	US-08-362-525-12	Sequence 12, Appl
2	672.5	23.5	574	US-10-023-515-4	Sequence 4, Appl
3	491.5	17.2	575	US-08-348-920-1	Sequence 1, Appl
4	488.5	17.1	575	US-08-348-920-2	Sequence 2, Appl
5	454	15.9	614	US-08-446-100-25	Sequence 25, Appl
6	452	15.8	600	US-08-370-156-4	Sequence 4, Appl
7	452	15.8	600	US-08-814-095-4	Sequence 4, Appl
8	452	15.8	600	US-08-975-084-1	Sequence 1, Appl
9	452	15.8	602	US-08-975-084-1	Sequence 1, Appl
10	452	15.8	602	5215909-11	Patent No. 5215909
11	452	15.8	614	US-07-732-962A-2	Sequence 2, Appl
12	452	15.8	614	US-08-370-156-2	Sequence 2, Appl
13	452	15.8	614	US-08-446-100-19	Sequence 19, Appl
14	452	15.8	614	US-08-446-100-21	Sequence 21, Appl
15	452	15.8	614	US-08-814-095-2	Sequence 2, Appl
16	452	15.8	614	PTC-US92-06106-2	Sequence 2, Appl
17	452	15.8	617	US-08-370-156-6	Sequence 6, Appl
18	452	15.8	617	US-08-814-095-6	Sequence 6, Appl
19	452	15.8	645	US-09-949-016-7063	Sequence 7063, Ap
20	452	15.8	645	US-09-949-016-7064	Sequence 7064, Ap
21	451	15.7	602	US-08-446-100-1	Sequence 1, Appl
22	451	15.7	602	US-08-446-100-24	Sequence 24, Appl
23	451	15.7	602	US-09-334-489-3	Sequence 3, Appl
24	451	15.7	602	US-09-334-489-4	Sequence 4, Appl
25	451	15.7	643	US-09-949-016-11146	Sequence 11146, A
26	449.5	15.7	572	US-08-932-376A-2	Sequence 2, Appl
27	449	15.7	602	US-08-446-100-13	Sequence 13, Appl

28	448	15.6	602	3	US-08-446-100-11	Sequence 11, Appl
29	447	15.6	602	3	US-08-446-100-3	Sequence 3, Appl
30	447	15.6	602	3	US-08-446-100-4	Sequence 4, Appl
31	447	15.6	602	3	US-08-446-100-5	Sequence 5, Appl
32	447	15.6	602	3	US-08-446-100-12	Sequence 12, Appl
33	447	15.6	602	3	US-08-446-100-15	Sequence 15, Appl
34	447	15.6	602	3	US-08-446-100-16	Sequence 16, Appl
35	447	15.6	602	3	US-08-446-100-17	Sequence 17, Appl
36	447	15.6	602	3	US-08-446-100-18	Sequence 18, Appl
37	447	15.6	614	3	US-08-446-100-22	Sequence 22, Appl
38	447	15.6	614	3	US-08-446-100-23	Sequence 23, Appl
39	446	15.6	602	3	US-08-446-100-8	Sequence 8, Appl
40	445	15.5	602	3	US-08-446-100-14	Sequence 14, Appl
41	444.5	15.5	544	2	US-08-932-376A-4	Sequence 4, Appl
42	444.5	15.5	635	6	5215909-10	Patent No. 5215909
43	444.5	15.5	635	6	5215909-10	Patent No. 5215909
44	444	15.5	614	3	US-08-446-100-20	Sequence 20, Appl
45	443	15.5	573	6	5215909-12	Patent No. 5215909

ALIGNMENTS

RESULT 1
US-08-362-525-12
; Sequence 12, Application US/08362525
; Patent No. 6027910
; GENERAL INFORMATION:
; APPLICANT: KLIS, FRANCISCUS M.
; APPLICANT: SCHREUDER, MAARTEN P.
; APPLICANT: TOSCHKA, HOLSER Y.
; APPLICANT: VERRIPS, CORNELIS T.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
; TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,525
; FILING DATE: 04-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92202080.5
; FILING DATE: 08-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92203899.7
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/01763
; FILING DATE: 07-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 213289/T7020(V)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 563 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-362-525-12

Query Match      38.7%; Score 1107; DB 3; Length 563;
Best Local Similarity 43.4%; Pred. No. 6.8e-100;
Matches 240; Conservative 73; Mismatches 196; Indels 44; Gaps 9;

QY 9  GRLGSVPTAKLANGDTITGLNAINIEAFLGIPAEPPVGNLRFKDPVPVSGSLNGQKFTS 68
Db 16  GTLAQAPTAVLANGNEVISGLGKVDYTFKGIIPADPPVGDLPFRKPPPTGSGYQGLKAND 75
QY 69  YGPGSCMOQNEPCTFE-----ENLKTALDLVMQSKVFAVLPOQSEDCLTINV 115
Db 76  FSSACMLDPGNFSLDKVGLKLPNLGRLPYDMA-----QGSVMNEDCLYNV 129
QY 116  VRPPGKTAGANLPLVLMWIFGGFEGISPTIFFPAQWTKSVLMGKHIIHVAVYRVASWG 175
Db 130  FRPAGTKPDALPLVMWIIYGGAFFGSSASYFGNGYKESVEMGQPVVVFVSINRTGPVG 189
QY 176  FLAGDDIKAGSGNAGLKQRLGMQWADNIAGFGDPSKVTIFGESAGSMSVLCHLIWN 235
Db 190  FLGGDAITAEGNTNAGLHQRLGLEWVSDNIANFGGDPDKVMIFGESAGAMVAHQLVAY 249
QY 236  DGDNTYKGPLFRAGIMQSGAMVPDPVDGTGNEYIDLFFVSSAGC---GSASDKLACL 292
Db 250  GGDNTYNGQLFHSAILQSGGLPYDPDSTSGVESAYSRFAQYAGCDTSASNDITLACL 309
QY 293  SASSDTLLDATNN-----TPGFLAYSSURLSYLPRPDGKNITDDMYKLVRDQKYAS 343
Db 310  SKSSDVLHSAQNSYDLKDLFPQLPQLGFG-----PRPDGNIIPDAAYELYRSGRYAK 362
QY 344  VPVIIGDQNDGCTIFGLSLNVTWNAQARAYKQSFHASDAEITLMAAYPQDITQOSP 403
Db 363  VPIYITGNQBEDTILAPVAINATTTTPHVKKWLKYICQASDASLDRVLSLPGSWSEGPS 422
QY 404  FDTGVNALTPOKFRISAVLGDLAFTHARRYFLNHFQGGTKYFSLSKOLSGL-PWGTGFH 462
Db 423  FRIGIUNALTPOKFRIAAIFTDLQLFQSPRVMNATKQVNRWYIATQLHNLVPLGTFH 482
QY 463  ANDIVWQDYL-LGSGSVIYNNAFIATPDLDPNTAGLLVNWPKYTSOSSQGNLMMINAL 521
Db 483  GSDLLFQYVYVLDGPSSA-YRRYFISFANHDDPNVGNLQQWDWYT---DAGKEMLIQIHWI 538
QY 522  GLYTGKONPRTAG 534
Db 539  GNSMRTDPRFIEG 551

RESULT 2
US-10-023-515-4
; Sequence 4, Application US/10023515
; Patent No. 6664091
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A. J.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence

US-10-023-515-4
Query Match      23.5%; Score 672.5; DB 4; Length 574;
Best Local Similarity 34.9%; Pred. No. 4.4e-57;
Matches 195; Conservative 76; Mismatches 195; Indels 93; Gaps 18;

QY 35  AFLGIPPAEPVPPVGNLRFKDPVPY----SGSLNGQKFTSYGPGSCMOQNEPTEENLGKTA 90
Db 19  SFLGIPYAEPPVGNLRFKAPQPYKEPWSVDLDA---TKYPSCLDQDDDFGSLSLD-KVA 74
QY 91  LDVWQSKVFOAVLPQSEDCLTINVVRPPGKTAGANLFLVLMWIFGGFEGISPTIFFPQAQ 150
Db 75  LKMLSLGNLKLVLGKLSEDCLYLVNVTPTKNTKPSKLPVWVWIIHGGMFGSGHSLPLSL 134
QY 151  MYTKSVLMGKHIIHVAVYRVASWGFLAGDDIKABGSGNAGLKQRLGMQWADNIAGFG 210
Db 135  YDGSLEAREGNVIVVINSYRLGFLGFLSTGDDKLPFGSGNYGLLDQRLALKWYQDNIAAFG 194
QY 211  GDPSKVTIFGESAGSMSVLCHLIWNDGNTYKGPLFRAGIMQSGA----MVPSPDPVDG 265
Db 195  GDNPSVTIFGESAGHASVSLLLSNGGNDPPSSKGLFHRAISQSGSALSPWAIQESNAR 254
QY 266  TYGNEYIDLFFVSSAGC---SASDKLACLRSASDITLLDATNNTPGLAYS-----SLRLS 318
Db 255  GRAKELARLL---GCNETSSSELLDCLRSKSAELLEATRS---FLLPEYVVPFLPLFLA 307
QY 319  YLPRPDGKN-----ITDDMYKLVRDQKYASVPVIIGDQNDGCTIFGLSLNVTWNAQAR- 372
Db 308  FGPVVDGDDAPEAFIPEDPEBELIKEGFADVPYLGIVTKDEGGYFAAMLLNASSKGEDEL 367
QY 373  -----AVFQKSPFHASDA-----EIDFLMAAYPQDITQSGSPFDTGVNALTTP 414
Db 368  KKETNPVWLELLKYLFLYASEALNIKMDLADLVLEKYPGDVDDFS-----VES 418
QY 415  QFKRISAVLGDLAF-----THARR-----YFLNHFQGGTKYFSLSKOLSGLPLIM 458
Db 419  RKPQLQDMLTDLFLKCPTRVAADLHAKHGSPVYAVYVDHPASFGIQGLAKRVDP-BFG 477
QY 459  GTFHANDI--VWQDYLL-----GSGSVIYNNAFIATPDLDPN--TAGLLVNW 502
Db 478  GAVHGEITFFVFGNPLKELKYKATEEBEESKSSKTMNYWANFAKTGNPNNGTSGLVWV 537
QY 503  PKYTSSSQSGNNLMMINAL 521
Db 538  PKYTSEEKYSLLILLTTI 556

RESULT 3
US-08-348-920-1
; Sequence 1, Application US/08348920
; Patent No. 5695750
; GENERAL INFORMATION:
; APPLICANT: Doctor, Bhupendra P.
; APPLICANT: Maxwell, Donald
; APPLICANT: Saxena, Ashima
; APPLICANT: Radic, Zoran
; APPLICANT: Taylor, Palmer
; TITLE OF INVENTION: Compositions for Use to Deactivate
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John F. Moran
; STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
; STREET: Detrick
; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,920
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: doc348,920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7807
; TELEFAX: 301-619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-348-920-1

Query Match 17.2%; Score 491.5; DB 1; Length 575;
Best Local Similarity 30.4%; Pred. No. 2.9e-39;
Matches 164; Conservative 75; Mismatches 195; Indels 105; Gaps 24;

QY 22 GDTITGLNAINAEFLGIPFAEPVGNLRFKDP-----VPYSGSLNGQKFTSYGSPSCMQNP 78
DB 17 GTRVPLVLSHIS-AFLGIPFAEPVGNMFRPEPKPWSGVWNAsty-----PNNCQV 71

QY 79 EGTFEENLGTALDLVMSQKVFQAVLPQSEDCLTINV-----VRPPTKAGANLPVLMWIF 134
DB 72 DEQFPFGSG-----SEMNNPREMSEDCLYLNIVPSPRKST-----TWVVIY 116

QY 135 GGGFEIGSPPTTPPPAQWTKSVLMGKH-----IIHVAIVRYASWGFLA--GDDIKAE 186
DB 117 GGGFYSGSSTL-----DVYNGKYLAYTEEVVLVSLSYRVGAFGLALHGSQ---EA 164

QY 187 SGNAGLKDOORLGMQWADNIAGFGDPKSVTIFGSAGSMVLCILWNGDNTYKGRPL 246
DB 165 PGNVGLLDQRMALQWHDNIQFFGDPKTVTFIGSAGSAGSVGMHIL-----SPGSRDL 218

QY 247 FRAGIMQSGAMVPSDP---VDGTYGNEYIDLVFVSSAGCGSASDK--LACLRASASD 301
DB 219 FRRLIQSGS--PNCFWASVSVAEGRRRAVELGRNLNCLNSDEBLIHLCKEKKQELID 276

QY 302 ATNTPGFLAYSSL-RLSYLPDPGKNIITDDMYKLVRDGKYASVPVIIGDQNDGTIFGL 360
DB 277 VEWNV---LPFDSIFRFSVPVIDGEFFPTSLMSLNSGNPKKTKILLGVNKGESFFIL 333

QY 361 -----SSLNVTNAQARAYFKOSFIHASDAEIDLMAAYPQDITQSPDPTGVNAL 412
DB 334 YGAPGFKDSKESKISREDPMGSKVLSVPHANDGLDAVTLQY-----TDMDDNNIGKR- 388

QY 413 TPQFKRISAVGLDLAFIHARRYFLN---HFQGGTKYSLSKLSGL---PINGTPHANDI 466
DB 389 -----DGLDDIVGDHNVICPLMFVNKYTKFGNGTYLIFENHRASNLVWPMGVHGYEI 444

QY 467 VMQDYLLGSGSVIYNN-----AFIATATDLDPTNA-GLLVNWPKYTSSQ 510
DB 445 ---EFVFGPLVKELNYTAEEALSRRIMHYWATFAKTGNPNPHEPQSKWPLFTTKEQ 500

RESULT 4
US-08-348-920-2
; Sequence 2, Application US/08348920
; Patent No. 5695750
; GENERAL INFORMATION:
; APPLICANT: Doctor, Bhupendra P.
; APPLICANT: Maxwell, Donald
; APPLICANT: Saxena, Ashima
; APPLICANT: Radic, Zoran

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; APPLICANT: Taylor, Palmer
; TITLE OF INVENTION: Compositions for Use to Deactivate
; ORGANOPHOSPHATES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John F. Moran
; STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,920
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: doc348,920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7807
; TELEFAX: 301-619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-348-920-2

Query Match 17.1%; Score 488.5; DB 1; Length 575;
Best Local Similarity 30.2%; Pred. No. 5.8e-39;
Matches 163; Conservative 76; Mismatches 195; Indels 105; Gaps 24;

QY 22 GDTITGLNAINAEFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGSPSCMQNP 78
DB 17 GTRVPLVLSHIS-AFLGIPFAEPVGNMFRPEPKPWSGVWNAsty-----PNNCQV 71

QY 79 EGTFEENLGTALDLVMSQKVFQAVLPQSEDCLTINV-----VRPPTKAGANLPVLMWIF 134
DB 72 DEQFPFGSG-----SEMNNPREMSEDCLYLNIVPSPRKST-----TWVVIY 116

QY 135 GGGFEIGSPPTTPPPAQWTKSVLMGKH-----IIHVAIVRYASWGFLA--GDDIKAE 186
DB 117 GGGFYSGSSTL-----DVYNGKYLAYTEEVVLVSLSYRVGAFGLALHGSQ---EA 164

QY 187 SGNAGLKDOORLGMQWADNIAGFGDPKSVTIFGSAGSMVLCILWNGDNTYKGRPL 246
DB 165 PGNVGLLDQRMALQWHDNIQFFGDPKTVTFIGSAGSAGSVGMHIL-----SPGSRDL 218

QY 247 FRAGIMQSGAMVPSDP---VDGTYGNEYIDLVFVSSAGCGSASDK--LACLRASASD 301
DB 219 FRRLIQSGS--PNCFWASVSVAEGRRRAVELGRNLNCLNSDEBLIHLCKEKKQELID 276

QY 302 ATNTPGFLAYSSL-RLSYLPDPGKNIITDDMYKLVRDGKYASVPVIIGDQNDGTIFGL 360
DB 277 VEWNV---LPFDSIFRFSVPVIDGEFFPTSLMSLNSGNPKKTKILLGVNKGESFFIL 333

QY 361 -----SSLNVTNAQARAYFKOSFIHASDAEIDLMAAYPQDITQSPDPTGVNAL 412
DB 334 YGAPGFKDSKESKISREDPMGSKVLSVPHANDGLDAVTLQY-----TDMDDNNIGKR- 388

QY 413 TPQFKRISAVGLDLAFIHARRYFLN---HFQGGTKYSLSKLSGL---PINGTPHANDI 466

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QY 86 LGKLTALDLVMSKVFQAVLPQSEDCLTINNVPRPGTKAGANLPVMLWIFGGGFEIGSPPTI 145
Db 119 PNREL-----SEDCLYLN-VMTYPRTPTSPVLVMIWYGGGFGYSGASL 161
QY 146 FPPAQWTKSVLMGXKHIIH-----VAVNYRVASMGFLAGDDIKAEKSGNAGLKQDRLQM 199
Db 162 -----DVGDFRFLVQAERTVLVSMNYRVGAFGLALPGSR-EAPGNVGLLDQRLAL 211
QY 200 QWVADNIAGFGDPKSVTIFGESAGSMVSLCHLIWNGDNTYKGPLFRAGIMQSGAMVP 259
Db 212 QWQENVAAGFGDPTSVTLFGESAGASVGMHLL-----SPSRGLFHRAVLQSGA--P 263
QY 260 SDPVDTGTG-----NEIYDLFVSSAGC-----GSASDKLACLRASSDPTLLDATNN 305
Db 264 NGPW-ATVGMGEARRRATQLAHL-----VGCPPGGTGGNDTELVACLRTPAQVLV---NH 315
QY 306 TPGFLAYSSL-RLSYLPRPDGKNITDDMYKLVRDGYASVPVLIIGDQNDGTFI----- 358
Db 316 EHHVLPOESVFRFSPVVDGDFLSDTPEALINAGDFHGLQVLGVVVDKDEGSYFLVYGAP 375
QY 359 GLSSLN--VTTNAQARAYFKQSFIIHASDAEIDTLMAAY-----POD-----ITQSPDFTGV 408
Db 376 GFSKDNESLISRAEFLAGVRVGPQVSDLAEEAVVLHYTDLWHPEDPARLREALSDVVDG 435
QY 409 LNALTPQFKRISAVLGDIAFIHAR--RYFLNHFG-----GTYKSFSLKQLSGLPT- 457
Db 436 HNVVCP-----VAQLAGRLAAQGARVYAYVFEHRASTLSWPLMWGVPHGHEIFIGIPLD 491
QY 458 -MGTFHANDIVWQDYLGGSGSVIYNNAFIATDLDNPTA--GLLVNPKYTSQQ 510
Db 492 PSRNYTAEKIFAQRLM-----RYWANFARTGDPNEPRDPKAPQPPYTAGAQ 539

RESULT 7

US-08-814-095-4
; Sequence 4, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-814-095-4
Query Match 15.8%; Score 452; DB 3; Length 600;
Best Local Similarity 29.1%; Pred. No. 2.5e-35;
Matches 156; Conservative 83; Mismatches 179; Indels 118; Gaps 26;
QY 35 AFLGIPFAEPVGNLRFKDP---VYSGSLNGKQFTSYGSPCMQ-----QNPETGFEEN 85
Db 62 AFLGIPFAEPVGNLRFKDP---VYSGSLNGKQFTSYGSPCMQ-----QNPETGFEEN 85
QY 86 LGKLTALDLVMSKVFQAVLPQSEDCLTINNVPRPGTKAGANLPVMLWIFGGGFEIGSPPTI 145
Db 119 PNREL-----SEDCLYLN-VMTYPRTPTSPVLVMIWYGGGFGYSGASL 161
QY 146 FPPAQWTKSVLMGXKHIIH-----VAVNYRVASMGFLAGDDIKAEKSGNAGLKQDRLQM 199
Db 162 -----DVGDFRFLVQAERTVLVSMNYRVGAFGLALPGSR-EAPGNVGLLDQRLAL 211
QY 200 QWVADNIAGFGDPKSVTIFGESAGSMVSLCHLIWNGDNTYKGPLFRAGIMQSGAMVP 259
Db 212 QWQENVAAGFGDPTSVTLFGESAGASVGMHLL-----SPSRGLFHRAVLQSGA--P 263
QY 260 SDPVDTGTG-----NEIYDLFVSSAGC-----GSASDKLACLRASSDPTLLDATNN 305
Db 264 NGPW-ATVGMGEARRRATQLAHL-----VGCPPGGTGGNDTELVACLRTPAQVLV---NH 315
QY 306 TPGFLAYSSL-RLSYLPRPDGKNITDDMYKLVRDGYASVPVLIIGDQNDGTFI----- 358
Db 316 EHHVLPOESVFRFSPVVDGDFLSDTPEALINAGDFHGLQVLGVVVDKDEGSYFLVYGAP 375
QY 359 GLSSLN--VTTNAQARAYFKQSFIIHASDAEIDTLMAAY-----POD-----ITQSPDFTGV 408
Db 376 GFSKDNESLISRAEFLAGVRVGPQVSDLAEEAVVLHYTDLWHPEDPARLREALSDVVDG 435
QY 409 LNALTPQFKRISAVLGDIAFIHAR--RYFLNHFG-----GTYKSFSLKQLSGLPT- 457
Db 436 HNVVCP-----VAQLAGRLAAQGARVYAYVFEHRASTLSWPLMWGVPHGHEIFIGIPLD 491
QY 458 -MGTFHANDIVWQDYLGGSGSVIYNNAFIATDLDNPTA--GLLVNPKYTSQQ 510
Db 492 PSRNYTAEKIFAQRLM-----RYWANFARTGDPNEPRDPKAPQPPYTAGAQ 539

RESULT 8

US-08-975-084-1
; Sequence 1, Application US/08975084
; Patent No. 6258780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: FRIEDMAN, Alon
; APPLICANT: SEIDMAN, Shlomo
; APPLICANT: KAUFER, Daniela
; TITLE OF INVENTION: A METHOD AND COMPOSITION FOR ENABLING
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6258780thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,084
; FILING DATE: 11-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.

```
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-975-084-1

Query Match      15.8%; Score 452; DB 3; Length 600;
Best Local Similarity 29.1%; Pred. No. 2.5e-35;
Matches 156; Conservative 83; Mismatches 179; Indels 118; Gaps 26;

QY 35 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGPSQMQ-----QNPFGTFFEN 85
Db 62 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGPSQMQ-----QNPFGTFFEN 118
QY 86 LGKTALDLVMSQKVFQAVLPQSEDCLTINNVVRP---PGTKAGANLPMVLWIFGGFEGSPTI 145
Db 119 FNREL-----SEDCLYLN-VWTPPRPTSPTPVVLWVWIFGGFEGSPTI 161
QY 146 FPPAQWTKSVLMGKHIIH-----VAVNRYVASWGFLAGDDIIKAEGSGNAGLKDQRLGM 199
Db 162 -----DVIDGRFLVQAERTVLVSMNRYVGAFFLALPGSR-EAPGVNGLLDQRLAL 211
QY 200 QWVADNIAGFGDPSKVTIFGESAGSMVSLCHLIWNGDNTYKGLPLFRAGIMQSGAMVP 259
Db 212 QWVQENVAAGFGDPTSVTLFGESAGASVSLHL-----SPPSRGLFHRVLOSQA--P 263
QY 260 SDVPDGTG-----NEIYDLFVSSAGC-----GSASDKLACLRSSASDTLLDATNN 305
Db 264 NGPW-ATVGMGARRRATQLAHL-----VGCPPGGTGNDTELVALCLTRPAQLV---NH 315
QY 306 TPGFLAYSSL-RLSLYLRPRDGNITDDMYKLVDRGKYASVPVVIIGDQNDGTFIF----- 358
Db 316 EHWLVPQESVFRFSFPVVDGDFLSDTPEALINAGDFHGLQVLGVVWVXDEGSYFLVYGAP 375
QY 359 GLSSLN--VTTNAQARAYFKQSFHASDAEIDTLMAY-----POD-----ITGSPFDTG 408
Db 376 GFSKONESLISRAEFLAGVRVGVQVPSDLAAEAVVLHYTDLWHPEDPARLREALSDVVYGD 435
QY 409 LNALTPQPKRISAVLGDLAFIHR--RYFLNHFG-----GTYGFLSKQLSGLPI- 457
Db 436 HNVVCP-----VAQLAGRLAAQARVAVYVFEHRASTLSWPLWMGVPHGYEIEFIFGIFLD 491
QY 458 -MGTTHANDIVMDYLLGGSGSVIYNNAFAFATDLPNTA--GLLVNMPKYYTSSSQ 510
Db 492 PSRNYTABEKIFAQRLM-----RYWANFARTGDPNEPRDPKAPQWPPTTAGAQ 539

RESULT 9
5215909-11
; Patent No. 5215909
; APPLICANT: SOREQ, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:11:
; LENGTH: 602
5215909-11

Query Match      15.8%; Score 452; DB 6; Length 602;
Best Local Similarity 29.5%; Pred. No. 2.5e-35;
Matches 158; Conservative 82; Mismatches 190; Indels 106; Gaps 25;

QY 22 GDTITGLNAINAEAFGLIPFAEPVGNLRFKDPVPYSGSLNGQKFTSYGPSQMQNPFGT 81
Db 50 GGTVT-----AFLGIPYAQPPLGRLRFKKQPSLTKWSDIWNATKYANSCC-QNIQDS 100
QY 82 FEENLGKTALDLVMSQKVFQAVLPQSEDCLTINNVVRP--PGTKAGANLPMVLWIFGGFEG 140
Db 101 FPGFHG-----SEMMNPTDLSDECLYLVNWI PAKPKP---NATVLIWYGGGQ 148
QY 141 GSPTIFPPPAQWTKSVLMGK-----HIIHVAVNRYVASWGFLAGDDIIKAEGSGNAGLK 194
Db 149 GTSSL-----HVDGKFLARVERVIVSMNRYVGALGFLAWPG-NPEAPGNMGLFD 198
QY 195 QRLGMQWADNIAGFGDPSKVTIFGESAGSMVSLCHLIWNGDNTYKGLPLFRAGIMQS 254
Db 199 QQLALQWQKNIAAPGPNKSVTLFGESAGASVSLHL-----LFTRAIIQS 252
QY 255 GAMVPSDPDGTG--GNEIYDLFVSSAGC--SASDKLACLRSSASDTLLDATNNTPGL 310
Db 253 GSFNAPWAVTSLYEARNETLNL-AKLTCGSRNETETI IKLRNKDPOBIL---LNEAFV 308
QY 311 AYSS-RLSLYLRPRDGNITDDMYKLVDRGKYASVPVVIIGDQNDGTFIF-----GLSSL 363
Db 309 PYGTPLSVNFGTVDGDFLTMDPDLLELQFKTKQILVGVNKGDEGTAFVYGAFGSKD 368
QY 364 N--VTTNAQARAYFKQSFHASDAEIDTLMAY-----PODITGSPFDTGVLNALT 413
Db 369 NNSIITRKEPQEGULKIPPGVSEFGKESILFHYTDWDDQRPENTREALGDVVDGYNFIC 428
QY 414 P--QFKRISAVLGDLAFIHRARYFLNHFGGTYKSYFLSKQLSGLPIMGTFHANDIWMODY 471
Db 429 PALBETKXFSWGNNAFP---YVFEH-----RSSKLPWPEWVMGVMHGYE1---EP 472
QY 472 LLG-----SGSVIYNNAFAFATDLPNTA--TAGLLVNWPKYYTSSSQ 510
Db 473 VFGLPLERRDNYTKABEILSRIV--KRWANFAKYGNFNETQNNSTSWPVFKSTEQ 526

RESULT 10
5215909-11
; Patent No. 5215909
; APPLICANT: SOREQ, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:11:
; LENGTH: 602
5215909-11

Query Match      15.8%; Score 452; DB 6; Length 602;
Best Local Similarity 29.5%; Pred. No. 2.5e-35;
Matches 158; Conservative 82; Mismatches 190; Indels 106; Gaps 25;

QY 22 GDTITGLNAINAEAFGLIPFAEPVGNLRFKDPVPYSGSLNGQKFTSYGPSQMQNPFGT 81
Db 50 GGTVT-----AFLGIPYAQPPLGRLRFKKQPSLTKWSDIWNATKYANSCC-QNIQDS 100
QY 82 FEENLGKTALDLVMSQKVFQAVLPQSEDCLTINNVVRP--PGTKAGANLPMVLWIFGGFEG 140
Db 101 FPGFHG-----SEMMNPTDLSDECLYLVNWI PAKPKP---NATVLIWYGGGQ 148
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QY 141 GSFTIPPPAQWYTKSVLMCK-----HHHVAVNVYASWGLAGDDIKAEAGSGNAGLKD 194
DB 149 GTSSL-----HVIDGKFLARVERVIVVSMYRVGALGLAWPG-NPEAPGNMGLFD 198
QY 195 ORLQWQVADNITAGGDPKVTIFGESAGSMVLCILWNGDNTYKGLPFRAGIMQS 254
DB 199 QQLALQWQVKNIAAGGNPKSVTLFESAGASVSLHL-LFTRAILQS 252
QY 255 GAMPSPDPVDGTY--GNEIYDLFVSSAGC--SASDKLACLARSASSDTLLDATNTPGFL 310
DB 253 GSFNAPWAVTSLYEARNLTNL-AKLTCGSRNETEIIKLRNKDPQEL--LNEAFV 308
QY 311 AYSS-LRLSYLPRPGKNITDMYKLRDGYKVASVPVIGDQNDGTIF-----GLSSL 363
DB 309 PYGTSLVNFPGTVDGDFLTPMDPILLELQPKTKQILVGVNKGDEGTAFLVYGAFGSKD 368
QY 364 N-VTTNAQARAYFKOSFIHASDAIDTLMAAY-----PQDITQSPDPVTGVLNALT 413
DB 369 NSIITRKEFQGLKIFPGVSEFGKESILFHYTDWDDQRPENYREALGDVVGDYNFIC 428
QY 414 P--QFKRISAVLGDLAFIHARRYFLNHFQGGTKYSFLSKQLSGLPIMGTFFHANDIWMODY 471
DB 429 PALETKKFESEGNNAFF-----YFEH-----RSSKLWPWPMWGMHGYEI--EP 472
QY 472 LLG-----SGSVIYNNAFIAPATOLDPN-TAGLLVNNPKYTSSEQ 510
DB 473 VFGLPLERRDNYTKAEILSRISIV--KRWANPAKYGNPNETQNNSTSNVPFKSTRQ 526

RESULT 11
US-07-732-962A-2
; Sequence 2, Application US/07732962A
; Patent No. 5248604
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07732,962A
; FILING DATE: 19910722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-732-962A-2

Query Match 15.8%; Score 452; DB 1; Length 614;
Best Local Similarity 29.1%; Pred. No. 2.5e-35;
Matches 156; Conservative 83; Mismatches 179; Indels 118; Gaps 26;

QY 35 AFLGIPFAEPVGNLRFKDP---VPYSGLSNGKQFTSYGSCMQ-----QNPEGTFFBN 85
DB 62 AFLGIPFAEPVGNLRFKDP---VPYSGLSNGKQFTSYGSCMQ-----QNPEGTFFBN 118
QY 86 LGKTALDLVMOSKVFQAVLPQSECLTINVRPCTKAGANLPMWLWIFGGFBEIGSPYI 145
DB 119 PNREL-----SEDCLYLN-VMTVPYPRPTSPTPVLVWYIYGGFYSGASSL 161
QY 146 FPPAQWTKSVLMCKHHI-----VAVNVYASWGLAGDDIKAEAGSGNAGLKDORLCM 199
DB 162 -----DVIDGRFLVQABRTVLVSMYRVGAFGLALPGSR-EAPGNVGLLDORLAL 211
QY 200 QWADNITAGGDPKVTIFGESAGSMVLCILWNGDNTYKGLPFRAGIMQSGAMVP 259
DB 212 QWQENVAAGFGDPTSVTLFESAGASVGMHLL-----SPPSRGLFHRVAVLQSGA--P 263
QY 260 SDPVDGTYG-----NEIYDLFVSSAGC-----GSASDKLACLARSASSDTLLDATNN 305
DB 264 NGPW-ATVGMGEARRATQLAHL-----VGCPPGGTGGNDTELVACLRTPAQVLV---NH 315
QY 306 TPGFLAYSSL-RLSYLPDPGKNITDDMYKLRDGYKVASVPVIGDQNDGTIF----- 358
DB 316 EWHVLPQESVPRFSPVVDGDFLSDTPEALINAGDFHGLQVLGVGVKDEGSYFLVYGAP 375
QY 359 GLSSLN--VTTNAQARAYFKOSFIHASDAIDTLMAAY-----PQDITQSPDPVTG 408
DB 376 GFSKDNESLSRAEFLAGVRVGVQVSDLAEEAVVLHYTDLWHPEDPARLEALSDVVGD 435
QY 409 LNALTPQPKRISAVLGDLAFIHAR--RYFLNHFQ-----GTYKYSFLSKQLSGLPT- 457
DB 436 HNVVCP-----VAQLAGRLAAQARVYAVVFHRASTLSWPLWGMVPHGYEIEFIFGILPD 491
QY 458 -MGTFFHANDIWMODYLLGSGSVIYNNAFIAPATOLDPN-TAGLLVNNPKYTSSEQ 510
DB 492 PSRNYTAEKIFAORLM-----RYWANPARTDNEPRDPKAPQMPYTAGAQ 539

RESULT 12
US-08-370-156-2
; Sequence 2, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Multford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-370-156-2

Query Match 15.8%; Score 452; DB 2; Length 614;
Best Local Similarity 29.1%; Pred. No. 2.5e-35;
Matches 156; Conservative 83; Mismatches 179; Indels 118; Gaps 26;

QY 35 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGPSQCMQ-----QNPGEFTFEEN 85
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QY 62 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGPSQCMQ-----QNPGEFTFEEN 118
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 86 LGKLTALDLVMSQKVFQAVLPQSEDCLTINVRPPTKAGANLPMVLMWIFGGFEGTSPTI 145
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 119 PNREL-----SEDCLYLN-VMTYPRPTSPPTPLVLMWYGGFYGSGASL 161
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 146 PPPAQWVTKSVLMGKHIIH-----VAVNYRVASMGFLAGDDIKAEGSGNAGLKDQRLGM 199
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 162 -----DVTGDFLQVQAEFTVLSMNYRVGAFGLALPGSR-EAPGNVGLLDQRLAL 211
QY 200 QWVADNIAAGFGDPSKVTIFGESAGSMVYLCHLIWNGDNTYKPKPLFRAGIMQSGAMVP 259
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 212 QWQENVAAGFGDPTSVTLFGESAGASVGMHLL-----SPSRGLFHRVAVLQSGA--P 263
QY 260 SDPVGVTVG-----NEIYDLFVSSAGC-----GSASDKLACLRASDSTLLDATNN 305
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 264 NGPW-ATVGMGEARRATQLAHL-----VGCPPGGTGGNDTELVACLRTPAQVLV--NH 315
QY 306 TPGFLAYSSL-RLSYLPRPDGKNITDDMYKLVRDCKYASVPVILGDQNDGTFI----- 358
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 316 EHWLVPQESVFRFSFVPVVDGDFLSDTPEALINAGDFHGLQVLGVVWDEGSYFLVYGAP 375
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QY 359 GLSSLN--VTNQAQARYFKQSFIHASDAEIDTLMAAY-----PQD---ITQGSPPFDTVG 408
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QY 376 GFSKDNESLISRAEFLAGVRVGPVQVSDLAABAVLHYTDLMLHPEDPARLREALSDVVGD 435
QY 409 LNALTPQFKRISAVLGDLAFTHAR--RYFLNHFGQ-----GTYKSFSLKQSLGLPI- 457
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 436 HNVVCP-----VAQLAGRLAAQARYVAYVFEHRASTLSWPLMWGVPVHGYEIEFIFGIPLD 491
QY 458 -MGTFHANDIWMQDYLLGSGSVIYNNAFIATATLDPNATA--GLLVNMPKYSSTSSQ 510
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 492 PSRNTAEKIFAQRLM-----RYWANPARTGDPNEPRDPKAPQPPPYTAGAQ 539
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RESULT 13
US-08-446-100-19
; Sequence 19, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-19

Query Match 15.8%; Score 452; DB 3; Length 614;
Best Local Similarity 29.1%; Pred. No. 2.5e-35;
Matches 156; Conservative 83; Mismatches 179; Indels 118; Gaps 26;

QY 35 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGPSQCMQ-----QNPGEFTFEEN 85
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QY 62 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGQKFTSYGPSQCMQ-----QNPGEFTFEEN 118
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 86 LGKLTALDLVMSQKVFQAVLPQSEDCLTINVRPPTKAGANLPMVLMWIFGGFEGTSPTI 145
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 119 PNREL-----SEDCLYLN-VMTYPRPTSPPTPLVLMWYGGFYGSGASL 161
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 146 PPPAQWVTKSVLMGKHIIH-----VAVNYRVASMGFLAGDDIKAEGSGNAGLKDQRLGM 199
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 162 -----DVTGDFLQVQAEFTVLSMNYRVGAFGLALPGSR-EAPGNVGLLDQRLAL 211
QY 200 QWVADNIAAGFGDPSKVTIFGESAGSMVYLCHLIWNGDNTYKPKPLFRAGIMQSGAMVP 259
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 212 QWQENVAAGFGDPTSVTLFGESAGASVGMHLL-----SPSRGLFHRVAVLQSGA--P 263
QY 260 SDPVGVTVG-----NEIYDLFVSSAGC-----GSASDKLACLRASDSTLLDATNN 305
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 264 NGPW-ATVGMGEARRATQLAHL-----VGCPPGGTGGNDTELVACLRTPAQVLV--NH 315
QY 306 TPGFLAYSSL-RLSYLPRPDGKNITDDMYKLVRDCKYASVPVILGDQNDGTFI----- 358
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 316 EHWLVPQESVFRFSFVPVVDGDFLSDTPEALINAGDFHGLQVLGVVWDEGSYFLVYGAP 375
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 359 GLSSLN--VTNQAQARYFKQSFIHASDAEIDTLMAAY-----PQD---ITQGSPPFDTVG 408
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QY 376 GFSKDNESLISRAEFLAGVRVGPVQVSDLAABAVLHYTDLMLHPEDPARLREALSDVVGD 435
QY 409 LNALTPQFKRISAVLGDLAFTHAR--RYFLNHFGQ-----GTYKSFSLKQSLGLPI- 457
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QY 436 HNVVCP-----VAQLAGRLAAQARYVAYVFEHRASTLSWPLMWGVPVHGYEIEFIFGIPLD 491
QY 458 -MGTFHANDIWMQDYLLGSGSVIYNNAFIATATLDPNATA--GLLVNMPKYSSTSSQ 510
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 492 PSRNTAEKIFAQRLM-----RYWANPARTGDPNEPRDPKAPQPPPYTAGAQ 539
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
US-08-446-100-21
; Sequence 21, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
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OM protein - protein search, using sw model

Run on: September 17, 2005, 07:49:54 ; Search time 172 Seconds
(without alignments)
1287.764 Million cell updates/sec

Title: US-09-943-857A-4
Perfect score: 2864
Sequence: 1 SMNSRGPAGRLGVSPTAKIA.....DNFRTAGYDALMTNPSPFFV 547

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues
Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2864	100.0	547	10 US-09-943-857-4	Sequence 4, Appli
2	2588	90.4	547	10 US-09-943-857-10	Sequence 10, Appl
3	2513	87.7	549	20 US-11-061-894-2	Sequence 2, Appli
4	2513	87.7	549	20 US-11-061-233-2	Sequence 2, Appli
5	2495	87.1	547	10 US-09-943-857-8	Sequence 8, Appli
6	2434	85.0	547	10 US-09-943-857-6	Sequence 6, Appli
7	2396	83.7	547	10 US-09-943-857-2	Sequence 2, Appli
8	1170.5	40.9	561	15 US-10-369-493-4236	Sequence 4236, Ap
9	674.5	23.6	612	9 US-09-875-353-4	Sequence 4, Appli
10	674.5	23.6	612	16 US-10-193-452-30	Sequence 30, Appl
11	672.5	23.5	574	13 US-10-023-515-4	Sequence 4, Appli

12	672.5	23.5	574	15	US-10-674-636-4	Sequence 4, Appli
13	664	23.2	585	9	US-09-934-323-4	Sequence 4, Appli
14	664	23.2	585	16	US-10-193-452-56	Sequence 56, Appl
15	484	16.9	576	18	US-10-503-643-3	Sequence 3, Appli
16	484	16.9	576	18	US-10-503-691-4	Sequence 4, Appli
17	482	16.8	574	9	US-09-748-739A-21	Sequence 21, Appl
18	482	16.8	574	14	US-10-032-233-48	Sequence 48, Appl
19	482	16.8	574	16	US-10-413-432-48	Sequence 48, Appl
20	482	16.8	574	16	US-10-324-466-48	Sequence 48, Appl
21	477	16.7	574	9	US-09-748-739A-23	Sequence 23, Appl
22	477	16.7	574	14	US-10-032-233-50	Sequence 50, Appl
23	477	16.7	574	16	US-10-413-432-50	Sequence 50, Appl
24	477	16.7	574	16	US-10-324-466-50	Sequence 50, Appl
25	459	16.0	574	9	US-09-748-739A-22	Sequence 22, Appl
26	459	16.0	574	14	US-10-032-233-49	Sequence 49, Appl
27	459	16.0	574	16	US-10-413-432-49	Sequence 49, Appl
28	459	16.0	574	16	US-10-324-466-49	Sequence 49, Appl
29	459	16.0	574	18	US-10-728-723-188	Sequence 188, App
30	458	16.0	574	18	US-10-728-723-164	Sequence 164, App
31	457	16.0	530	18	US-10-728-723-204	Sequence 204, App
32	457	16.0	574	18	US-10-728-723-178	Sequence 178, App
33	457	16.0	574	18	US-10-728-723-180	Sequence 180, App
34	457	16.0	574	18	US-10-728-723-184	Sequence 184, App
35	457	16.0	765	18	US-10-728-723-202	Sequence 202, App
36	456	15.9	574	14	US-10-032-233-40	Sequence 40, Appl
37	456	15.9	574	16	US-10-413-432-40	Sequence 40, Appl
38	456	15.9	574	16	US-10-324-466-40	Sequence 40, Appl
39	456	15.9	574	18	US-10-728-723-32	Sequence 32, Appl
40	456	15.9	574	18	US-10-728-723-74	Sequence 74, Appl
41	455	15.9	574	9	US-09-748-739A-8	Sequence 8, Appli
42	455	15.9	574	18	US-10-728-723-42	Sequence 42, Appl
43	455	15.9	574	18	US-10-728-723-114	Sequence 114, App
44	455	15.9	574	18	US-10-728-723-186	Sequence 186, App
45	454	15.9	574	18	US-10-728-723-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-943-857-4
; Sequence 4, Application US/09943857
; Publication No. US20030124701A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Jei-Fu
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Yue
; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943,857
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Candida rugosa
; US-09-943-857-4

Query Match 100.0%; Score 2864; DB 10; Length 547;
Best Local Similarity 100.0%; Pred. No. 1e-250;
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SMNSRGPAGRLGVSPTAKLANGDITITGNALINEAFGLIPFAEPVGNLRKDPVPYSGS	60
Db	1	SMNSRGPAGRLGVSPTAKLANGDITITGNALINEAFGLIPFAEPVGNLRKDPVPYSGS	60
Qy	61	LNQKFTSYGSCMQQPEGTFFENLKTALDLVQSKVFOAVLPQSDCLITINVRPPG	120
Db	61	LNQKFTSYGSCMQQPEGTFFENLKTALDLVQSKVFOAVLPQSDCLITINVRPPG	120
Qy	121	TKAGANLPVMLWIFGGGFEIGSPITFPPAQMTKSVLMGKHIIHVANNRYRVASMGFLAGD	180

Db 121 TRAGANLPVLMWIFGGGFEIGSPTIPPPAQMVTKSVLMGKHIIHVAVNVRVASWGFLAGD 180
Qy 181 DIKAECSGNAGLKDORLQWQWADNIAGFGDPBSKVTIEGESAGSMVSLCHLIWNGDNT 240
Db 181 DIKAECSGNAGLKDORLQWQWADNIAGFGDPBSKVTIEGESAGSMVSLCHLIWNGDNT 240
Qy 241 YKGKPLFRAGIMQSGAMVPSDPVDGTYGNEIYDLFVSSAGCGSASDKLACLSASDITLL 300
Db 241 YKGKPLFRAGIMQSGAMVPSDPVDGTYGNEIYDLFVSSAGCGSASDKLACLSASDITLL 300
Qy 301 DATNNTPGFLAYSSRLSYLPRPDGKNIITDDMYKLVROGKYASVPVIGDQNDGDTIFGL 360
Db 301 DATNNTPGFLAYSSRLSYLPRPDGKNIITDDMYKLVROGKYASVPVIGDQNDGDTIFGL 360
Qy 361 SSLNVTNNAQARAYFKQSFHSDAEIDTLMMAYPQDITQGSPPFTGVNLALTPOFKRIS 420
Db 361 SSLNVTNNAQARAYFKQSFHSDAEIDTLMMAYPQDITQGSPPFTGVNLALTPOFKRIS 420
Qy 421 AVLGDLAFIHARRYFLNHFQGGTKYSLKQSLGSLPIMGTFFHANDIWMQDYLLGSGSVIY 480
Db 421 AVLGDLAFIHARRYFLNHFQGGTKYSLKQSLGSLPIMGTFFHANDIWMQDYLLGSGSVIY 480
Qy 481 NNAFTAFATDLDPTAGLLVNNPKYTSSSQSGNNLMINALGLYTKONFRTAGYDALMT 540
Db 481 NNAFTAFATDLDPTAGLLVNNPKYTSSSQSGNNLMINALGLYTKONFRTAGYDALMT 540
Qy 541 NPSSSPFV 547
Db 541 NPSSSPFV 547

RESULT 2
US-09-943-857-10
; Sequence 10, Application US/09943857
; Publication No. US20030124701A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Jei-Fu
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Jye
; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943,857
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Candida rugosa
US-09-943-857-10

Query Match 90.4%; Score 2588; DB 10; Length 547;
Best Local Similarity 88.7%; Pred. No. 1.2e-225;
Matches 485; Conservative 30; Mismatches 22; Indels 0; Gaps 0;
Qy 1 SMNSRGPAGRLGVSPTAKLANGDTITGLNAINAEFLGIPPAEPVGNLRFKDPVPYSGS 60
Db 1 SMNSRGPAGRLGVSPTATLANGDTITGLNAINAEFLGIPPAEPVGNLRFKDPVPYSGS 60
Qy 61 LMGKFTSYGSCMQONPEGTFEENLTKTALDLVMQSKVFOAVLPQSEDCLTINVRPPG 120
Db 61 LDGQFTSYGSCMQONPEGTYEENLTKAALDLVMQSKVFEAVSPSEDCLTINVRPPG 120
Qy 121 TRAGANLPVLMWIFGGGFEIGSPTIPPPAQMVTKSVLMGKHIIHVAVNVRVASWGFLAGD 180
Db 121 TRAGANLPVLMWIFGGGFEIGSPTIPPPAQMTKSIAMGKPIIHVSNVRVSSWGFLAGD 180
Qy 181 DIKAECSGNAGLKDORLQWQWADNIAGFGDPBSKVTIEGESAGSMVSLCHLIWNGDNT 240
Db 181 EIKAECSANAGLKDQWQWADNIAGFGDPKVTIEGESAGSMVSLCHLIWNGDNT 240
Qy 241 YKGKPLFRAGIMQSGAMVPSDPVDGTYGNEIYDLFVSSAGCGSASDKLACLSASDITLL 300

Db 241 YKGKPLFRAGIMQSGAMVPSDAVDGVYGNIEFDLLASDAGCGSADKLACLRGVSSDTLE 300
Qy 301 DATNNTPGFLAYSSRLSYLPRPDGKNIITDDMYKLVROGKYASVPVIGDQNDGDTIFGL 360
Db 301 DATNNTPGFLAYSSRLSYLPRPDGKNIITDDMFALVREGKYASVPVIGDQNDGDTIFGT 360
Qy 361 SSLNVTNNAQARAYFKQSFHSDAEIDTLMMAYPQDITQGSPPFTGVNLALTPOFKRIS 420
Db 361 SSLNVTNNAQARAYFKQSFHSDAEIDTLMMAYPQDITQGSPPFTGVNLALTPOFKRIS 420
Qy 421 AVLGDLAFIHARRYFLNHFQGGTKYSLKQSLGSLPIMGTFFHANDIWMQDYLLGSGSVIY 480
Db 421 AVLGDLAFIHARRYFLNHFQGGTKYSLKQSLGSLPIMGTFFHANDIWMQDYLLGSGSVIY 480
Qy 481 NNAFTAFATDLDPTAGLLVNNPKYTSSSQSGNNLMINALGLYTKONFRTAGYDALMT 540
Db 481 NNAFTAFATDLDPTAGLLVNNPKYETSSSQSGNNLMINALGLYTKONFRTAGYDALFS 540
Qy 541 NPSSSPFV 547
Db 541 NPSSSPFV 547

RESULT 3
US-11-061-894-2
; Sequence 2, Application US/11061894
; Publication No. US20050188439A1
; GENERAL INFORMATION:
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Abad, Andre R.
; TITLE OF INVENTION: Methods for Enhancing Insect Resistance
; FILE REFERENCE: 035718/286812
; CURRENT APPLICATION NUMBER: US/11/061,894
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,845
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: 60/546,533
; PRIOR FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Lipase from C. cylindracea
US-11-061-894-2

Query Match 87.7%; Score 2513; DB 20; Length 549;
Best Local Similarity 87.5%; Pred. No. 7.8e-219;
Matches 470; Conservative 32; Mismatches 35; Indels 0; Gaps 0;
Qy 11 LGSVPTAKLANGDTITGLNAINAEFLGIPPAEPVGNLRFKDPVPYSGSLNGQKFTSYG 70
Db 13 VAAAPTATLANGDTITGLNAINAEFLGIPPAEPVGNLRFKDPVPYSGSLDGQKFTSYG 72
Qy 71 PSCMQONPEGTFEENLTKTALDLVMQSKVFOAVLPQSEDCLTINVRPPGTAGANLPM 130
Db 73 PSCMQONPEGTYEENLTKAALDLVMQSKVFEAVSPSEDCLTINVRPPGTAGANLPM 132
Qy 131 LWIFGGGFEIGSPTIPPPAQMVTKSVLMGKHIIHVAVNVRVASWGFLAGDDIKAGSGNA 190
Db 133 LWIFGGGFEIGSPTIPPPAQMTKSIAMGKPIIHVSNVRVSSWGFLAGDEIKAGSANA 192
Qy 191 GLKQRLQWQWADNIAGFGDPBSKVTIEGESAGSMVSLCHLIWNGDNTYKGPFLFRAG 250
Db 193 GLKQRLQWQWADNIAGFGDPKVTIEGESAGSMVSLCHLIWNGDNTYKGPFLFRAG 252
Qy 251 IMQSGAMVPSDPVDGTYGNEIYDLFVSSAGCGSASDKLACLSASDITLLDATNNTPGFL 310
Db 253 IMQSGAMVPSDAVDGIYGNIEFDLLASNAGCGSASDKLACLRGVSSDTLEATNNTPGFL 312

Qy	311	AYSSLRLSYLP	RPD	GKNI	TDD	MYLVR	GK	YAS	VP	VI	GQND	EGT	I	FG	LS	IN	TT	NAQ	370
Db	313	AYSSLRLSYLP	RPD	GKNI	TDD	MYLVR	GK	YAS	VP	VI	GQND	EGT	I	FG	LS	IN	TT	NAQ	372
Qy	371	ARAYFKQSGFI	HAS	DAE	IDT	LMAA	YPO	DI	TQGS	PFDT	GVL	NALT	PO	PKR	IS	AV	IG	LAF	430
Db	373	AREYFKQSGFV	HAS	DAE	IDT	LMTA	YPO	DI	TQGS	PFDT	GVL	NALT	PO	PKR	IS	AV	IG	LAF	432
Qy	431	ARRYFLNHFO	G	G	T	K	Y	S	P	L	S	K	Q	L	S	G	L	P	490
Db	433	ARRYFLNHYT	G	G	T	K	Y	S	P	L	S	K	Q	L	S	G	L	P	492
Qy	491	LDPNTAGLLV	NWPK	YTS	SSQ	S	G	NNI	LM	IN	AL	GL	Y	T	G	K	ON	FR	547
Db	493	LDPNTAGLLV	NWPK	YTS	SSQ	S	G	NNI	LM	IN	AL	GL	Y	T	G	K	ON	FR	549

RESULT 4

```

US-11-061-233-2
; Sequence 2, Application US/11061233
; Publication No. US20050198706A1
; GENERAL INFORMATION:
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Abad, Andre R.
; APPLICANT: Wong, James F.
; APPLICANT: Yu, Guo Cao
; TITLE OF INVENTION: Lipases and Methods of Use
; FILE REFERENCE: 035718/286811
; CURRENT APPLICATION NUMBER: US/11/061,233
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,605
; PRIOR FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic lipase from C. cylindracea
US-11-061-233-2

```

[illegible]

RESULT 5

```

US-09-943-857-8
; Sequence 8, Application US/09943857
; Publication No. US20030124701A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Jai-Fu
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Jye
; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943,857
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Candida rugosa
US-09-943-857-8

```

	Query Match	87.18	Score 2495	DB 10	Length 547	
	Best Local Similarity	86.3	Pred. No. 3.3e-217			
	Matches 472	Conservative 31	Mismatches 44	Indels 0	Gaps 0	
Qy	1	SMNSRGPAGRLGVSPTAKLANGDTITGLNAIINEAFLGIPFAEPVVGMLRKPDPVPYRGS	60			
Db	1	SMNSRGPAGRLGVSPTATLANGDTITGLNAIINEAFLGIPFAEPVVGMLRKPDPVPYRGS	60			
Qy	61	LNQOKTYSYGPSQMOQPEGTFFENLCKTALDLVMQSKVFOAVLPQSDCDCTINVRPPG	120			
Db	61	LNQGSFTAYGPSQMOQPEGTFFENLCKVALDLVMQSKVFOAVLPNSDCTINVRPPG	120			

RESULT 6

US-09-943-857-6

; Sequence 6, Application US/09943857

; Publication No. US20030124701A1

; GENERAL INFORMATION:

; APPLICANT: Shaw, Jei-Fu

; APPLICANT: Lee, Guan-Chiun

; APPLICANT: Tang, Shye-Jye

; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES

; FILE REFERENCE: 08919-066001

; CURRENT APPLICATION NUMBER: US/09/943,857

; CURRENT FILING DATE: 2001-08-31

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 547

; TYPE: PRT

; ORGANISM: Candida rugosa

US-09-943-857-6

Query Match 85.0%; Score 2434; DB 10; Length 547;

Best Local Similarity 83.5%; Pred. No. 1.1e-211;

Matches 457; Conservative 38; Mismatches 52; Indels 0; Gaps 0;

```
QY 1 SMNSRGPAGRLGVSPTAKLANGDTTITGLNAIINEAFLGIPPAEPPVGNLRPKDPVPYSGS 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 SMNSRGPAGRLGVSPTATLANGDTTITGLNAIINEAFLGIPPAEPPVGNLRPKDPVPYSGS 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 LMGQFTSYGSCMQNPGTEENLKTALDLVMQSKVQAVLPQSEDCLTINVRPPG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 LMGQFTSYGSCMQNPGTEENLKTALDLVMQSKVQAVLPQSEDCLTINVRPPG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 TRAGANLPVWLWIFGGGFEIGSPITPPPAQMTVKSVMGKHIIHVAVNRYRVASWGLAGD 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 TRAGANLPVWLWIFGGGFEIGSSLPFAQMITASVLMGKPIIHVSMNRYRVASWGLAGP 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 DIKAEGSGNAGLKDORLGMQWADNIAGFGDPSPKVTIIFGESAGSMSVLCHLIWNDGNT 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 DIKAEGSGNAGLKDORLGMQWADNIAGFGDPSPKVTIIFGESAGSMSVNCQLLWNDGNT 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 YGKGLPFRAGIMQSGAMVPSDPVDTGYGNEIYDLFVSSAGCGSASDKLACLRSSDITLL 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 YGKGLPFRAGIMQSGAMVPSDPVDTGYGNEIYDLFVSSAGCGSASDKLACLRSSDITLL 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 DATNTPGLAYSSRLSYLSPRPDGKNIITDDMYKLVRDGKYASVPVIIGDQNDGTTIFGL 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 301 QATSDTPGALAYPSRLSFLPRPDGTFITDDMYKLVRDGKCANVPVIIGDQNDGTTIFGL 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 SSLNVTNQAARAYPKQSFHASDAEIDTLMAAYPQDITQGSPPFTGTGVLNALTPOPKRIS 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 361 SSLNVTNQAARAYPKQSFHASDAEIDTLMAAYPQDITQGSPPFTGTGVLNALTPOPKRIS 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 AVLGDLAFTLARRYFLNHFQGGTKYFSLSKQLSGLPIMGTTHANDIWMQDYLGGSGVY 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 421 AVLGDLAFTLARRYFLNHFQGGTKYFSLSKQLSGLPIMGTTHANDIWMQDYLGGSGVY 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 481 NNAFTAFATDLPNTAGLLVNNPKYTSSSQSGNNLMINALGLYTGKDNFRTAGYDALMT 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 481 NNAFTAFANDLPNKAGLLVNNPKYTSSSQSGNNLMINALGLYTGKDNFRTAGYDALMT 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 541 NPSSPFV 547
| | | | |
DB 541 NPSSPFV 547
| | | | |
```

RESULT 7

US-09-943-857-2

; Sequence 2, Application US/09943857

; Publication No. US20030124701A1

; GENERAL INFORMATION:

; APPLICANT: Shaw, Jei-Fu

```
; APPLICANT: Lee, Guan-Chiun
; APPLICANT: Tang, Shye-Jye
; TITLE OF INVENTION: RECOMBINANT CANDIDA RUGOSA LIPASES
; FILE REFERENCE: 08919-066001
; CURRENT APPLICATION NUMBER: US/09/943,857
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Candida rugosa
US-09-943-857-2
```

Query Match 83.7%; Score 2396; DB 10; Length 547;

Best Local Similarity 82.3%; Pred. No. 3.2e-208;

Matches 450; Conservative 34; Mismatches 63; Indels 0; Gaps 0;

```
QY 1 SMNSRGPAGRLGVSPTAKLANGDTTITGLNAIINEAFLGIPPAEPPVGNLRPKDPVPYSGS 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 SMNSRGPAGRLGVSPTATLANGDTTITGLNAIINEAFLGIPPAEPPVGNLRPKDPVPYSGS 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 LMGQFTSYGSCMQNPGTEENLKTALDLVMQSKVQAVLPQSEDCLTINVRPPG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 LMGQFTSYGSCMQNPGTEENLKTALDLVMQSKVQAVLPQSEDCLTINVRPPG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 TRAGANLPVWLWIFGGGFEIGSPITPPPAQMTVKSVMGKHIIHVAVNRYRVASWGLAGD 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 TRAGANLPVWLWIFGGGFEIGSSLPFAQMITASVLMGKPIIHVSMNRYRVASWGLAGP 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 DIKAEGSGNAGLKDORLGMQWADNIAGFGDPSPKVTIIFGESAGSMSVLCHLIWNDGNT 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 DIKAEGSGNAGLKDORLGMQWADNIAGFGDPSPKVTIIFGESAGSMSVTFVHLVWNDGNT 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 YGKGLPFRAGIMQSGAMVPSDPVDTGYGNEIYDLFVSSAGCGSASDKLACLRSSDITLL 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 YGKGLPFRAGIMQSGAMVPSDPVDTGYGNEIYDLFVSSAGCGSASDKLACLRSSDITLL 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 DATNTPGLAYSSRLSYLSPRPDGKNIITDDMYKLVRDGKYASVPVIIGDQNDGTTIFGL 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 301 QATSDTPGALAYPSRLSFLPRPDGTFITDDMYKLVRDGKCANVPVIIGDQNDGTTIFGL 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 SSLNVTNQAARAYPKQSFHASDAEIDTLMAAYPQDITQGSPPFTGTGVLNALTPOPKRIS 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 361 SSLNVTNQAARAYPKQSFHASDAEIDTLMAAYPQDITQGSPPFTGTGVLNALTPOPKRIS 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 AVLGDLAFTLARRYFLNHFQGGTKYFSLSKQLSGLPIMGTTHANDIWMQDYLGGSGVY 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 421 AVLGDLAFTLARRYFLNHFQGGTKYFSLSKQLSGLPIMGTTHANDIWMQDYLGGSGVY 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 481 NNAFTAFATDLPNTAGLLVNNPKYTSSSQSGNNLMINALGLYTGKDNFRTAGYDALMT 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 481 NNAFTAFANDLPNKAGLLVNNPKYTSSSQSGNNLMINALGLYTGKDNFRTAGYDALMT 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 541 NPSSPFV 547
| | | | |
DB 541 NPSSPFV 547
| | | | |
```

RESULT 8

US-10-369-493-4236

; Sequence 4236, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493


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; PRIOR APPLICATION NUMBER: US 60/199,559
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/862,556
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: PCT/US01/16424
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/206,036
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/861,165
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: PCT/US01/16014
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,442
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/875,353
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18335
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,949
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/896,578
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/20880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/214,948
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/911,150
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: PCT/US01/23153
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,008
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 09/911,317
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: PCT/US01/23160
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,040
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 09/934,323
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26091
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,774
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/963,959
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: PCT/US01/29962
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/235,033
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 09/971,490
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US01/31674
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/238,170
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/071,275
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: PCT/US02/03793
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/267,054
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 09/888,911
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/US01/19967
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,688
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 612
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-193-452-30

Query Match      23.6%; Score 674.5; DB 16; Length 612;
Best Local Similarity 34.0%; Pred. No. 7,5e-52;
Matches 199; Conservative 80; Mismatches 203; Indels 103; Gaps 19;

QY 19 LANGDTITGLNAINNE-----AFLGIPFARPPVGNLRFKDPVPY----SSSLNQ 64
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
31 VATNNVLCGKVRGVNNEKTDNGEQSVYSFLGIPYARPPVGNLRFKAPQYKPEPWSVDLDA- 89
QY 65 KFTSYGPGSCMQNPETGEENLGKLTALDLVWQSKVQFQAVLPQSEDECLINVRPGETKAG 124
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
90 --TRYPPSCLODDDFGFSLDL-KVALKWLGLWNKVLGLKLSDECLINVTTPKTPKN 146
QY 125 ANLPVLMWIFGGGFEIGSPITFPPAQMVTKSLVGMKHIHVAVNRYRVASWGLAGDDIKA 184
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
147 SKLPVWVIHGGGFPMFGSGHSLPLSLYDGESLAREGNVIVSYNRYRLGFLSTGDDXL 206
QY 185 EGSNAGLKDQRLGMQWVADNIAGFGDPKSVTTFGESAGSMVLCILINWDGDNTRYKKG 244
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
207 PGSGNYGLDQRLALKWVDNIAAFGGDPNSVTTFGESAGAASVSLLLSLNGDNPSPSK 266
QY 245 PLFRAGIMOSGA-----WVPSDPVDGTGNYEIYDLFVSSAGG--SASDKLACLRASSD 297
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
267 GLFHRAISQSGSALSFWAIQESNARGAKELARLL-----GCNETSSBELLDCLRSKSAE 322
QY 298 TLLDATNTNTPGFLAYS-----SLRSLYLRPDGKN-----ITDDMYKLVRDGKYASVPVI 347
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
323 ELLEATRS---FLLFEEYVFLPLFLAFGVPVDDGDAPEAFIPEDPEELIKGKPADVPYL 379
QY 348 IGDQDEGTIFGLSSLNVTNNAQR-----AYFKOSFIHASDA-----BID 388
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
380 IGVTKDEGGYFAAMLNASSKGEDELKKTNPVWLELLKYLFLFYASEALNIKOMDDLAD 439
QY 389 TLMAAYPODITQSGSPFDGVLNALTPOPKRISAVIGDLAF-----IHARR----- 433
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
440 KVLEKIPGVDVDFS-----VESRKNPQDDMLTDLFLKCPTRVAADLHAKHGGSVPY 490
QY 434 -YFLNHFQGGTKYFSLKSLGSLPIMGTFTHANDI--VMQDYLL-----GSGSV 478
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
491 AYPFDHPASFGIGQFLACKRVDP-EFGGAVHGDIEFFVFGNPLLKELQLYKATEEEKSSSK 549
QY 479 IYNNAFIATDLPN--TAGLLVNWPKYTSOSSQSGNNLMINAL 521
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
550 TMWNYWANFAKTGNPNNGTSNGLVVPKYSSEQKYSLLILLITTI 594

RESULT 11
US-10-023-515-4
; Sequence 4, Application US/10023515
; Publication No. US20020182636A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Consensus sequence
US-10-023-515-4

Query Match 23.5%; Score 672.5; DB 13; Length 574;
Best Local Similarity 34.9%; Pred. No. 1e-51;
Matches 195; Conservative 76; Mismatches 195; Indels 93; Gaps 18;

QY 35 AFLGIPFAEPPVGNLRFKDPVPY-----SGSLNGQKFTSYGSPCMQONPEGTFEENLGKTA 90
DB 19 SFLGIPYAEPPVGNLRFKAPQYKPEWSDVDA---TKYPPSCLQDDDFGFSLSL-KVA 74
QY 91 LDLVMSKVFOAVLPQSEDCLTINVVPRPGTKAGANLPMWLIFGCGPFIIGSTPTIPPPAQ 150
DB 75 LKMLSLGMNKLVLGSLSDCLVLYNTPKNTKPSKLPVWVWIHGGGFMFGSGHSLPLSL 134
QY 151 MYTKSLMGKHLIHVAVNRYVASWGLAGDDIKAEKSGNAGLKDORLGMOWADNITAGFG 210
DB 135 YDGEISLAREGNVIVSINRYLPGFLSTGDDKLPFGSGNYGLDORLALKWQDNIAPFG 194
QY 211 GDPKVTIFGESAGSMVLCILWNGDNTYKGLFRAGIMQSGA-----MVPDPVVDG 265
DB 195 GDPNSVTIFGESAGAASVSLLLSNGDNPSPSSKGLFHRAISQSGSALSPPWAIQESNAR 254
QY 266 TYGNEIYDLFVSSAGCG--SASDKLACLRSSASDITLLDATNTPGFLAYS-----SLRLS 318
DB 255 GRAKELARLL---GCNETSSSELLDCLRSKSAELLEATRS---FLLFEYVVPFLFLA 307
QY 319 YLPRPDGKN-----ITDDMYKLVRGKYASVPVIGDQNDGCTIFGLSSLNVTNAQAR- 372
DB 308 FGPVVDGDDAPFAFIPEDPEELIKEGKADVPYLGVTKDEGGYFAAMLLNASSKGEDEL 367
QY 373 -----AYFKQSFIHASDA-----EIDTLMAAYPQDITQGGSPFDGTGVLNALTTP 414
DB 368 KKETNPVWLELLKYLFFYASEALNIKMDDLADKLVLEKYPGDVDDFS-----VES 418
QY 415 QPKRISAVLGDLAF-----IHARR-----YFLNHFGGKYFSLSKLSGLPLIM 458
DB 419 RKPQLQDMLTDLFLKCPTRVAADLHAKHGGSPVYAYVFDHPASFGIGQFLAKRVDP-BFG 477
QY 459 GTFHANDI--VWQDYLL-----GSGSVIYNNAFIATDLDPN--TAGLLVNW 502
DB 478 GAVHGEIFFVFGNPLLEKQLYKATEEBEKSSTKTMNYANFAKTGNPNNGTNGLVVW 537
QY 503 PKYTSSSQSGNNLMINAL 521
DB 538 PKYTSEEKYSLLILTTI 556

RESULT 12
US-10-674-636-4
; Sequence 4, Application US/10674636
; Publication No. US20040086922A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/674,636
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/10/923,515
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Consensus sequence
US-10-674-636-4

Query Match 23.5%; Score 672.5; DB 15; Length 574;
Best Local Similarity 34.9%; Pred. No. 1e-51;
Matches 195; Conservative 76; Mismatches 195; Indels 93; Gaps 18;

QY 35 AFLGIPFAEPPVGNLRFKDPVPY-----SGSLNGQKFTSYGSPCMQONPEGTFEENLGKTA 90
DB 19 SFLGIPYAEPPVGNLRFKAPQYKPEWSDVDA---TKYPPSCLQDDDFGFSLSL-KVA 74
QY 91 LDLVMSKVFOAVLPQSEDCLTINVVPRPGTKAGANLPMWLIFGCGPFIIGSTPTIPPPAQ 150
DB 75 LKMLSLGMNKLVLGSLSDCLVLYNTPKNTKPSKLPVWVWIHGGGFMFGSGHSLPLSL 134
QY 151 MYTKSLMGKHLIHVAVNRYVASWGLAGDDIKAEKSGNAGLKDORLGMOWADNITAGFG 210
DB 135 YDGEISLAREGNVIVSINRYLPGFLSTGDDKLPFGSGNYGLDORLALKWQDNIAPFG 194
QY 211 GDPKVTIFGESAGSMVLCILWNGDNTYKGLFRAGIMQSGA-----MVPDPVVDG 265
DB 195 GDPNSVTIFGESAGAASVSLLLSNGDNPSPSSKGLFHRAISQSGSALSPPWAIQESNAR 254
QY 266 TYGNEIYDLFVSSAGCG--SASDKLACLRSSASDITLLDATNTPGFLAYS-----SLRLS 318
DB 255 GRAKELARLL---GCNETSSSELLDCLRSKSAELLEATRS---FLLFEYVVPFLFLA 307
QY 319 YLPRPDGKN-----ITDDMYKLVRGKYASVPVIGDQNDGCTIFGLSSLNVTNAQAR- 372
DB 308 FGPVVDGDDAPFAFIPEDPEELIKEGKADVPYLGVTKDEGGYFAAMLLNASSKGEDEL 367
QY 373 -----AYFKQSFIHASDA-----EIDTLMAAYPQDITQGGSPFDGTGVLNALTTP 414
DB 368 KKETNPVWLELLKYLFFYASEALNIKMDDLADKLVLEKYPGDVDDFS-----VES 418
QY 415 QPKRISAVLGDLAF-----IHARR-----YFLNHFGGKYFSLSKLSGLPLIM 458
DB 419 RKPQLQDMLTDLFLKCPTRVAADLHAKHGGSPVYAYVFDHPASFGIGQFLAKRVDP-BFG 477
QY 459 GTFHANDI--VWQDYLL-----GSGSVIYNNAFIATDLDPN--TAGLLVNW 502
DB 478 GAVHGEIFFVFGNPLLEKQLYKATEEBEKSSTKTMNYANFAKTGNPNNGTNGLVVW 537
QY 503 PKYTSSSQSGNNLMINAL 521
DB 538 PKYTSEEKYSLLILTTI 556

RESULT 13
US-09-934-323-4
; Sequence 4, Application US/09934323
; Patent No. US20020150910A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-081001
; CURRENT APPLICATION NUMBER: US/09/934,323
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,774
; PRIOR FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-09-934-323-4
Query Match 23.2%; Score 664; DB 9; Length 585;
Best Local Similarity 34.0%; Pred. No. 6.3e-51;


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Db 3 VATNVLCVKVGVNEKTDNGEQSVVYFGLGIYAEPPVGNLRFKAPQPYKEPWSVLDLA- 61
Qy 65 KFTSYGPSQCMQNPGETFBEENLKTALDLVMSQKVFQAVLPQSECLTINVVRPPTKAG 124
Db 62 ---TKYPPSCLQDDRGFSLDL-KVALKMLSGWKLKVLKLSLSECLYLVNVTPTKNTKPN 118
Qy 125 ANLPWMLWIFGGGFFIGSPITPPAQMVTKSVLMGKHIIHVAIVRVASWGLAGDDIKA 184
Db 119 SKLPVWVIHGGGFFGSGHSLPLSLYDGESLAREGNVIVINRYLPLGLFLSTGDDKL 178
Qy 185 EGSNGAG-LKQORLGMOWADNIAAGFGDPKVTIFGESAGSMVLCILINWGDNTYKG 243
Db 179 PGSGNYGLLDORLALKWQDNIAPFGDPNSVTIFGESAGAASVSLLLSNGGDNPPSS 238
Qy 244 KPLFRAGIMQSGA-----MVPDPVDGTGYNBIYDLFVSSAGCG--SASDKLACLRSSAS 296
Db 239 KGLFHRAISQSGSALSPPAIQESNARGRAKELARLL---GCNETSSSELLDCLRSKA 294
Qy 297 DTLLDATNTPGFLAYS-----SLRLSYLPRPDGKN-----ITDDMYKLVDRDGKYASVPV 346
Db 295 BELLEATRS---FLLFXYVPLPLFLAFGPVVVDGDAPEAFIPEDPELIKEGKPADVPY 351
Qy 347 IIGDQNDGRTIFGLSSLVNNTNAQAR-----AVFKOSFIHASDA-----EI 387
Db 352 LIGVTYKDEGYPFAAMLLNASSGKEDLKEKTNPDVWLELLKYLFPYASEALNIDMDLLA 411
Qy 388 DTLMAAYPQDITQGSFPDGTGVNLTALTPQKRISAVIGDLAF-----IHARR----- 433
Db 412 DKVLEKYPGDVDDPS-----VESRKPNIQDMLTDLLFKCPTFVAADLHAKHGSPV 462
Qy 434 ---YFLNHFGGTYKYSFLSKQSLGSLPIMGTFFHANDI--VWQDYLL-----GSGS 477
Db 463 YAYVFDHPASFGIGQFLAKRVDP-BFGGAVHGDIEFFVFGNPLKQELKATEBEKSSS 521
Qy 478 VIYNNAFTAFATDLPN--TAGLLVNWPKYTSQSGNNLMMINAL 521
Db 522 KTMNYWANFAKTGNPNNGTNGSLVWVWPKYTSSEQKYSLILLITTI 567

RESULT 15
US-10-503-643-3
; Sequence 3, Application US/10503643
; Publication No. US20050176117A1
; GENERAL INFORMATION:
; APPLICANT: Robyn Joyce Russell
; APPLICANT: Rama Heidari
; APPLICANT: Alan Devonshire
; APPLICANT: Susan Jane Dorrian
; APPLICANT: John Graham Oakeshott
; TITLE OF INVENTION: Degradation of hydrophobic ester pesticides and toxins
; FILE REFERENCE: 69-04
; CURRENT APPLICATION NUMBER: US/10/503,643
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/AU02/00114
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Torpedo californica
US-10-503-643-3

Query Match 16.9%; Score 484; DB 18; Length 576;
Best Local Similarity 30.6%; Pred. No. 1.3e-34;
Matches 160; Conservative 73; Mismatches 192; Indels 98; Gaps 23;

Qy 35 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGKQKFTSYGPSQCMQNPGETFBEENLKTAL 91
Db 30 AFLGIPFAEPVGNLRFKDP---VPYSGSLNGKQKFTSYGPSQCMQNPGETFBEENLKTAL 81
Qy 92 DLVMSQKVFQAVLPQSECLTINV-VRPDPGKAGANLPLVWIFGGGFEIGSPITFFPAQ 150
```

```
Db 82 -----SEMNPNREMSDCLYLNIVWPSRPRKSAT---VMLWIYGGGYSGSSTL----- 128
Qy 151 MVTKSVLMGKH-----LIHVAVNVRVASWGLA--GDDIKAEKSGNAGLKQORLGMOWV 202
Db 129 -----DVYNGKYLAYTEEVVLSLTVRGAFGLALHGSQ---EAPENMGLLDORVALQWV 181
Qy 203 ADNTAGFGGDPKSVTIPOGESAGSMVLCILINWGDNTYKGLKPLFRAGIMQSGAMVPSDP 262
Db 182 HDNIQFGGDPKVTITLFGESAGRASVGMHIL-----SPGSRDLFRALILQSGS--PNC 233
Qy 263 ---VDGTYGNEIYDLFVSSAGCGSASDK--LACLRASASDTLLDATNTPGFLAYSRL-R 316
Db 234 WASVSAEGRRAVELRENLCNLSRDLIQCRLREKPKQBELIDYEMNV---LPFDSIFR 290
Qy 317 LSYLPRPDGKNITDDMYKLVDRDGKYASVPVLIIGDQNDGRTIFGL-----SSLNVTTN 368
Db 291 PSFVPIVDEGFPPTSLESMLNAGNFKTKQIILGVNKGDEGSPFLLYGAGFGSKDSKISR 350
Qy 369 AQARAYFKQSFIHASDAEIDTLMAAYPQDITQGSFPDGTGVNLTALTPQKRISAVIGDLAF 428
Db 351 EDFMSGVKLSVPHANDLGLDAVTILQY---TDWMDNNGIKNR-----DGLDDIVGNHNV 401
Qy 429 IHARRYFLN---HFQGGTKYSFLSKQLSGL---PIWGTFFHANDIYVWQDYLLGSGSVIYNN 482
Db 402 ICPLMHFVNYKTKFGNGTYLYFFNHRASNLVWPEWMMGVHGYEI---BFFVGLPLVKELN 458
Qy 483 -----AFTAFATDLPNTA--GLLVNWPKYTSSSQ 510
Db 459 YTAEEALSRIMHYWATFATGNPNPHEPSQSKWPLFTTKEQ 501
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Search completed: September 17, 2005, 08:04:13
Job time : 174 secs

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